

MAIL ROOM  
FEB 7 1997  
SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: QUENTIN-MILLET, Marie-Jose et al.
- (ii) TITLE OF INVENTION: TBP2 FRAGMENTS OF THE TRANSFERRIN RECEPTOR OF NEISSERIA MENINGITIDIS
- (iii) NUMBER OF SEQUENCES: 42
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: LARSON AND TAYLOR
  - (B) STREET: 727 SOUTH 23RD STREET
  - (C) CITY: ARLINGTON
  - (D) STATE: VIRGINIA
  - (E) COUNTRY: USA
  - (F) ZIP: 22202
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER: US 08/591,447
  - (B) FILING DATE: 29-JAN-1996
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: SARRO, THOMAS P
  - (B) REGISTRATION NUMBER: 19,196
  - (C) REFERENCE/DOCKET NUMBER: XI/P02956
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: 703-920-7200
  - (B) TELEFAX: 703-892-8428

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2230 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: Neisseria meningitidis
  - (B) STRAIN: IM2169

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 60..119

(ix) FEATURE:

(A) NAME/KEY: mat\_peptide  
(B) LOCATION: 120..2192

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 60..2192

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION: 120..1154

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION: 1155..1748

(ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION: 1749..2192

(ix) FEATURE:

(A) NAME/KEY: misc\_binding  
(B) LOCATION: 237..1169

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATTGTGTTAAA AATAAATAAAA ATAATAATCC TTATCATTTCT TTAATTGAAT TGGGTTTAT 59

ATG AAC AAT CCA TTG GTA AAT CAG GCT GCT ATG GTG CTG CCT GTG TTT 107  
Met Asn Asn Pro Leu Val Asn Gln Ala Ala Met Val Leu Pro Val Phe  
-20 -15 -10 -5

TTG TTG AGT GCC TGT CTG GGC GGC GGC GGC AGT TTC GAT CTT GAT TCT 155  
Leu Leu Ser Ala Cys Leu Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser  
1 5 10

GTC GAT ACC GAA GCC CCG CGT CCC GCG CCA AAG TAT CAA GAT GTT TCT 203  
Val Asp Thr Glu Ala Pro Arg Pro Ala Pro Lys Tyr Gln Asp Val Ser  
15 20 25

TCC GAA AAA CCG CAA GCC CAA AAA GAC CAA GGC GGA TAC GGT TTT GCG 251  
Ser Glu Lys Pro Gln Ala Gln Lys Asp Gln Gly Gly Tyr Gly Phe Ala  
30 35 40

ATG AGG TTG AAA CGG AGG AAT TGG TAT CCG GGG GCA GAA GAA AGC GAG 299  
Met Arg Leu Lys Arg Arg Asn Trp Tyr Pro Gly Ala Glu Glu Ser Glu  
45 50 55 60

GTT AAA CTG AAC GAG AGT GAT TGG GAG GCG ACG GGA TTG CCG ACA AAA	347
Val Lys Leu Asn Glu Ser Asp Trp Glu Ala Thr Gly Leu Pro Thr Lys	
65 70 75	
CCC AAG GAA CTT CCT AAA CGG CAA AAA TCG GTT ATT GAA AAA GTA GAA	395
Pro Lys Glu Leu Pro Lys Arg Gln Lys Ser Val Ile Glu Lys Val Glu	
80 85 90	
ACA GAC GGC GAC AGC GAT ATT TAT TCT TCC CCC TAT CTC ACA CCA TCA	443
Thr Asp Gly Asp Ser Asp Ile Tyr Ser Ser Pro Tyr Leu Thr Pro Ser	
95 100 105	
AAC CAT CAA AAC GGC AGC GCT GGC AAC GGT GTA AAT CAA CCT AAA AAT	491
Asn His Gln Asn Gly Ser Ala Gly Asn Gly Val Asn Gln Pro Lys Asn	
110 115 120	
CAG GCA ACA GGT CAC GAA AAT TTC CAA TAT GTT TAT TCC GGT TGG TTT	539
Gln Ala Thr Gly His Glu Asn Phe Gln Tyr Val Tyr Ser Gly Trp Phe	
125 130 135 140	
TAT AAA CAT GCA GCG AGT GAA AAA GAT TTC AGT AAC AAA AAA ATT AAG	587
Tyr Lys His Ala Ala Ser Glu Lys Asp Phe Ser Asn Lys Lys Ile Lys	
145 150 155	
TCA GGC GAC GAT GGT TAT ATC TTC TAT CAC GGT GAA AAA CCT TCC CGA	635
Ser Gly Asp Asp Gly Tyr Ile Phe Tyr His Gly Glu Lys Pro Ser Arg	
160 165 170	
CAA CTT CCT GCT TCT GGA AAA GTT ATC TAC AAA GGT GTG TGG CAT TTT	683
Gln Leu Pro Ala Ser Gly Lys Val Ile Tyr Lys Gly Val Trp His Phe	
175 180 185	
GTA ACC GAT ACA AAA AAG GGT CAA GAT TTT CGT GAA ATT ATC CAG CCT	731
Val Thr Asp Thr Lys Lys Gly Gln Asp Phe Arg Glu Ile Ile Gln Pro	
190 195 200	
TCA AAA AAA CAA GGC GAC AGG TAT AGC GGA TTT TCT GGT GAT GGC AGC	779
Ser Lys Lys Gln Gly Asp Arg Tyr Ser Gly Phe Ser Gly Asp Gly Ser	
205 210 215 220	
GAA GAA TAT TCC AAC AAA AAC GAA TCC ACG CTG AAA GAT GAT CAC GAG	827
Glu Glu Tyr Ser Asn Lys Asn Glu Ser Thr Leu Lys Asp Asp His Glu	
225 230 235	
GGT TAT GGT TTT ACC TCG AAT TTA GAA GTG GAT TTC GGC AAT AAG AAA	875
Gly Tyr Gly Phe Thr Ser Asn Leu Glu Val Asp Phe Gly Asn Lys Lys	
240 245 250	
TTG ACG GGT AAA TTA ATA CGC AAT AAT GCG AGC CTA AAT AAT AAT ACT	923
Leu Thr Gly Lys Leu Ile Arg Asn Asn Ala Ser Leu Asn Asn Asn Thr	
255 260 265	

B  
cont.

AAT Asn 270	AAT Asn 270	GAC Asp	AAA Lys	CAT His	ACC Thr	ACC Thr	CAA Gln	TAC Tyr	TAC Tyr	AGC Ser	CTT Leu	GAT Asp	GCA Ala	CAA Gln	ATA Ile	971
ACA Thr 285	GGC Gly	AAC Asn	CGC Arg	TTC Phe	AAC Asn	GGC Gly	ACG Thr	GCA Ala	ACG Thr	GCA Ala	ACT Thr	GAC Asp	AAA Lys	AAA Lys	GAG Glu	1019
AAT Asn	GAA Glu	ACC Thr	AAA Lys	CTA Leu	CAT His	CCC Pro	TTT Phe	GTT Val	TCC Ser	GAC Asp	TCG Ser	TCT Ser	TCT Ser	TTG Leu	AGC Ser	1067
GGC Gly	GGC Gly	TTT Phe	TTC Phe	GGC Gly	CCG Pro	CAG Gln	GGT Gly	GAG Glu	GAA Glu	TTG Leu	GGT Gly	TTC Phe	CGC Arg	TTT Phe	TTG Leu	1115
AGC Ser	GAC Asp	GAT Asp	CAA Gln	AAA Lys	GTT Val	GCC Ala	GTT Val	GTC Val	GGC Gly	AGC Ser	GCG Ala	AAA Lys	ACC Thr	AAA Lys	GAC Asp	1163
AAA Lys 350	CTG Leu	GAA Glu	AAT Asn	GGC Gly	GCG Ala	GCG Ala	GCT Ala	TCA Ser	GGC Gly	AGC Ser	ACA Thr	GGT Gly	GCG Ala	GCA Ala	GCA Ala	1211
TCG Ser	GGC Gly	GGT Gly	GCG Ala	GCA Ala	GGC Gly	ACG Thr	TCG Ser	TCT Ser	GAA Glu	AAC Asn	AGT Ser	AAG Lys	CTG Leu	ACC Thr	ACG Thr	1259
GTT Val	TTG Leu	GAT Asp	GCG Ala	GTT Val	GAA Glu	TTG Leu	ACA Thr	CTA Leu	AAC Asn	GAC Asp	AAG Lys	AAA Lys	ATC Ile	AAA Lys	AAT Asn	1307
CTC Leu	GAC Asp	AAC Asn	TTC Phe	AGC Ser	AAT Asn	GCC Ala	GCC Ala	CAA Gln	CTG Leu	GTT Val	GTC Val	GAC Asp	GGC Gly	ATT Ile	ATG Met	1355
ATT Ile	CCG Pro	CTC Leu	CTG Leu	CCC Pro	AAG Lys	GAT Asp	TCC Ser	GAA Glu	AGC Ser	GGG Gly	AAC Asn	ACT Thr	CAG Gln	GCA Ala	GAT Asp	1403
AAA Lys 430	GGT Gly	AAA Lys	AAC Asn	GGC Gly	GGA Gly	ACA Thr	GAA Glu	TTT Phe	ACC Thr	CGC Arg	AAA Lys	TTT Phe	GAA Glu	CAC His	ACG Thr	1451
CCG Pro 445	GAA Glu	AGT Ser	GAT Asp	AAA Lys	AAA Lys	GAC Asp	GCC Ala	CAA Gln	GCA Ala	GGT Gly	ACG Thr	CAG Gln	ACG Thr	AAT Asn	GGG Gly	1499
GCG Ala	CAA Gln	ACC Thr	GCT Ala	TCA Ser	AAT Asn	ACG Thr	GCA Ala	GGT Gly	GAT Asp	ACC Thr	AAT Asn	GGC Gly	AAA Lys	ACA Thr	AAA Lys	1547

ACC	TAT	GAA	GTC	GAA	GTC	TGC	TGT	TCC	AAC	CTC	AAT	TAT	CTG	AAA	TAC	1595
Thr	Tyr	Glu	Val	Glu	Val	Cys	Cys	Ser	Asn	Leu	Asn	Tyr	Leu	Lys	Tyr	
		480						485					490			
GGA	ATG	TTG	ACG	CGC	AAA	AAC	AGC	AAG	TCC	GCG	ATG	CAG	GCA	GGA	GGA	1643
Gly	Met	Leu	Thr	Arg	Lys	Asn	Ser	Lys	Ser	Ala	Met	Gln	Ala	Gly	Gly	
		495					500					505				
AAC	AGT	AGT	CAA	GCT	GAT	GCT	AAA	ACG	GAA	CAA	GTT	GAA	CAA	AGT	ATG	1691
Asn	Ser	Ser	Gln	Ala	Asp	Ala	Lys	Thr	Glu	Gln	Val	Glu	Gln	Ser	Met	
	510					515					520					
TTC	CTC	CAA	GGC	GAG	CGT	ACC	GAT	GAA	AAA	GAG	ATT	CCA	ACC	GAC	CAA	1739
Phe	Leu	Gln	Gly	Glu	Arg	Thr	Asp	Glu	Lys	Glu	Ile	Pro	Thr	Asp	Gln	
	525				530					535					540	
AAC	GTC	GTT	TAT	CGG	GGG	TCT	TGG	TAC	GGG	CAT	ATT	GCC	AAC	GGC	ACA	1787
Asn	Val	Val	Tyr	Arg	Gly	Ser	Trp	Tyr	Gly	His	Ile	Ala	Asn	Gly	Thr	
				545					550					555		
AGC	TGG	AGC	GGC	AAT	GCT	TCT	GAT	AAA	GAG	GGC	GGC	AAC	AGG	GCG	GAA	1835
Ser	Trp	Ser	Gly	Asn	Ala	Ser	Asp	Lys	Glu	Gly	Gly	Asn	Arg	Ala	Glu	
			560					565					570			
TTT	ACT	GTG	AAT	TTT	GCC	GAT	AAA	AAA	ATT	ACC	GGC	AAG	TTA	ACC	GCT	1883
Phe	Thr	Val	Asn	Phe	Ala	Asp	Lys	Lys	Ile	Thr	Gly	Lys	Leu	Thr	Ala	
		575					580					585				
GAA	AAC	AGG	CAG	GCG	CAA	ACC	TTT	ACC	ATT	GAG	GGA	ATG	ATT	CAG	GGC	1931
Glu	Asn	Arg	Gln	Ala	Gln	Thr	Phe	Thr	Ile	Glu	Gly	Met	Ile	Gln	Gly	
		590				595					600					
AAC	GGC	TTT	GAA	GGT	ACG	GCG	AAA	ACT	GCT	GAG	TCA	GGT	TTT	GAT	CTC	1979
Asn	Gly	Phe	Glu	Gly	Thr	Ala	Lys	Thr	Ala	Glu	Ser	Gly	Phe	Asp	Leu	
	605				610					615					620	
GAT	CAA	AAA	AAT	ACC	ACC	CGC	ACG	CCT	AAG	GCA	TAT	ATC	ACA	GAT	GCC	2027
Asp	Gln	Lys	Asn	Thr	Thr	Arg	Thr	Pro	Lys	Ala	Tyr	Ile	Thr	Asp	Ala	
				625				630						635		
AAG	GTA	AAG	GGC	GGT	TTT	TAC	GGG	CCT	AAA	GCC	GAA	GAG	TTG	GGC	GGA	2075
Lys	Val	Lys	Gly	Gly	Phe	Tyr	Gly	Pro	Lys	Ala	Glu	Glu	Leu	Gly	Gly	
			640				645						650			
TGG	TTT	GCC	TAT	CCG	GGC	GAT	AAA	CAA	ACG	GAA	AAG	GCA	ACA	GCT	ACA	2123
Trp	Phe	Ala	Tyr	Pro	Gly	Asp	Lys	Gln	Thr	Glu	Lys	Ala	Thr	Ala	Thr	
		655					660					665				
TCC	AGC	GAT	GGA	AAT	TCA	GCA	AGC	AGC	GCG	ACC	GTG	GTA	TTC	GGT	GCG	2171
Ser	Ser	Asp	Gly	Asn	Ser	Ala	Ser	Ser	Ala	Thr	Val	Val	Phe	Gly	Ala	
		670				675					680					

6  
cont.

AAA CGC CAA CAG CCT GTG CAA TAAGCACGGT TGCCGAACAA TCAAGAATAA  
Lys Arg Gln Gln Pro Val Gln  
685 690

2222

GGCTTCAG

2230

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 711 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Asn Asn Pro Leu Val Asn Gln Ala Ala Met Val Leu Pro Val Phe  
-20 -15 -10 -5

Leu Leu Ser Ala Cys Leu Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser  
1 5 10

Val Asp Thr Glu Ala Pro Arg Pro Ala Pro Lys Tyr Gln Asp Val Ser  
15 20 25

Ser Glu Lys Pro Gln Ala Gln Lys Asp Gln Gly Gly Tyr Gly Phe Ala  
30 35 40

Met Arg Leu Lys Arg Arg Asn Trp Tyr Pro Gly Ala Glu Glu Ser Glu  
45 50 55 60

Val Lys Leu Asn Glu Ser Asp Trp Glu Ala Thr Gly Leu Pro Thr Lys  
65 70 75

Pro Lys Glu Leu Pro Lys Arg Gln Lys Ser Val Ile Glu Lys Val Glu  
80 85 90

Thr Asp Gly Asp Ser Asp Ile Tyr Ser Ser Pro Tyr Leu Thr Pro Ser  
95 100 105

Asn His Gln Asn Gly Ser Ala Gly Asn Gly Val Asn Gln Pro Lys Asn  
110 115 120

Gln Ala Thr Gly His Glu Asn Phe Gln Tyr Val Tyr Ser Gly Trp Phe  
125 130 135 140

Tyr Lys His Ala Ala Ser Glu Lys Asp Phe Ser Asn Lys Lys Ile Lys  
145 150 155

Ser Gly Asp Asp Gly Tyr Ile Phe Tyr His Gly Glu Lys Pro Ser Arg  
160 165 170

Gln	Leu	Pro	Ala	Ser	Gly	Lys	Val	Ile	Tyr	Lys	Gly	Val	Trp	His	Phe		
		175					180					185					
Val	Thr	Asp	Thr	Lys	Lys	Gly	Gln	Asp	Phe	Arg	Glu	Ile	Ile	Gln	Pro		
	190					195					200						
Ser	Lys	Lys	Gln	Gly	Asp	Arg	Tyr	Ser	Gly	Phe	Ser	Gly	Asp	Gly	Ser		
205					210					215					220		
Glu	Glu	Tyr	Ser	Asn	Lys	Asn	Glu	Ser	Thr	Leu	Lys	Asp	Asp	His	Glu		
				225					230					235			
Gly	Tyr	Gly	Phe	Thr	Ser	Asn	Leu	Glu	Val	Asp	Phe	Gly	Asn	Lys	Lys		
			240						245				250				
Leu	Thr	Gly	Lys	Leu	Ile	Arg	Asn	Asn	Ala	Ser	Leu	Asn	Asn	Asn	Thr		
		255					260					265					
Asn	Asn	Asp	Lys	His	Thr	Thr	Gln	Tyr	Tyr	Ser	Leu	Asp	Ala	Gln	Ile		
		270				275					280						
Thr	Gly	Asn	Arg	Phe	Asn	Gly	Thr	Ala	Thr	Ala	Thr	Asp	Lys	Lys	Glu		
285					290					295					300		
Asn	Glu	Thr	Lys	Leu	His	Pro	Phe	Val	Ser	Asp	Ser	Ser	Ser	Leu	Ser		
				305					310					315			
Gly	Gly	Phe	Phe	Gly	Pro	Gln	Gly	Glu	Glu	Leu	Gly	Phe	Arg	Phe	Leu		
			320					325					330				
Ser	Asp	Asp	Gln	Lys	Val	Ala	Val	Val	Gly	Ser	Ala	Lys	Thr	Lys	Asp		
		335					340					345					
Lys	Leu	Glu	Asn	Gly	Ala	Ala	Ala	Ser	Gly	Ser	Thr	Gly	Ala	Ala	Ala		
		350				355						360					
Ser	Gly	Gly	Ala	Ala	Gly	Thr	Ser	Ser	Glu	Asn	Ser	Lys	Leu	Thr	Thr		
365					370					375					380		
Val	Leu	Asp	Ala	Val	Glu	Leu	Thr	Leu	Asn	Asp	Lys	Lys	Ile	Lys	Asn		
				385					390					395			
Leu	Asp	Asn	Phe	Ser	Asn	Ala	Ala	Gln	Leu	Val	Val	Asp	Gly	Ile	Met		
			400					405					410				
Ile	Pro	Leu	Leu	Pro	Lys	Asp	Ser	Glu	Ser	Gly	Asn	Thr	Gln	Ala	Asp		
		415					420					425					
Lys	Gly	Lys	Asn	Gly	Gly	Thr	Glu	Phe	Thr	Arg	Lys	Phe	Glu	His	Thr		
		430				435					440						
Pro	Glu	Ser	Asp	Lys	Lys	Asp	Ala	Gln	Ala	Gly	Thr	Gln	Thr	Asn	Gly		
445					450					455					460		

B. cont.

Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly Lys Thr Lys  
465 470 475

Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr Leu Lys Tyr  
480 485 490

Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln Ala Gly Gly  
495 500 505

Asn Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln Val Glu Gln Ser Met  
510 515 520

Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro Thr Asp Gln  
525 530 535 540

Asn Val Val Tyr Arg Gly Ser Trp Tyr Gly His Ile Ala Asn Gly Thr  
545 550 555

Ser Trp Ser Gly Asn Ala Ser Asp Lys Glu Gly Gly Asn Arg Ala Glu  
560 565 570

Phe Thr Val Asn Phe Ala Asp Lys Lys Ile Thr Gly Lys Leu Thr Ala  
575 580 585

Glu Asn Arg Gln Ala Gln Thr Phe Thr Ile Glu Gly Met Ile Gln Gly  
590 595 600

*Bj.*  
Asn Gly Phe Glu Gly Thr Ala Lys Thr Ala Glu Ser Gly Phe Asp Leu  
605 610 615 620

Asp Gln Lys Asn Thr Thr Arg Thr Pro Lys Ala Tyr Ile Thr Asp Ala  
625 630 635

Lys Val Lys Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Leu Gly Gly  
640 645 650

Trp Phe Ala Tyr Pro Gly Asp Lys Gln Thr Glu Lys Ala Thr Ala Thr  
655 660 665

Ser Ser Asp Gly Asn Ser Ala Ser Ser Ala Thr Val Val Phe Gly Ala  
670 675 680

Lys Arg Gln Gln Pro Val Gln  
685 690

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1808 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)



(vi) ORIGINAL SOURCE:

- (A) ORGANISM: N. meningitidis  
(B) STRAIN: IM2394

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: 1..60

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide  
(B) LOCATION: 61..1797

(ix) FEATURE:

- (A) NAME/KEY: CDS  
(B) LOCATION: 1..1797

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
(B) LOCATION: 61..1035

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
(B) LOCATION: 1036..1386

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
(B) LOCATION: 1387..1797

(ix) FEATURE:

- (A) NAME/KEY: misc\_binding  
(B) LOCATION: 46..1050

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATG AAC AAT CCA TTG GTA AAT CAG GCT GCT ATG GTG CTG CCT GTG TTT 48  
Met Asn Asn Pro Leu Val Asn Gln Ala Ala Met Val Leu Pro Val Phe  
-20 -15 -10 -5

TTG TTG AGT GCT TGT CTG GGT GGC GGC GGC AGT TTC GAT TTG GAC AGC 96  
Leu Leu Ser Ala Cys Leu Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser  
1 5 10

GTG GAA ACC GTG CAA GAT ATG CAC TCC AAA CCT AAG TAT GAG GAT GAA 144  
Val Glu Thr Val Gln Asp Met His Ser Lys Pro Lys Tyr Glu Asp Glu  
15 20 25

AAA AGC CAG CCT GAA AGC CAA CAG GAT GTA TCG GAA AAC AGC GGC GCG 192  
Lys Ser Gln Pro Glu Ser Gln Gln Asp Val Ser Glu Asn Ser Gly Ala  
30 35 40

GCT TAT GGC TTT GCA GTA AAA CTA CCT CGC CGG AAT GCA CAT TTT AAT 240  
Ala Tyr Gly Phe Ala Val Lys Leu Pro Arg Arg Asn Ala His Phe Asn  
45 50 55 60

CCT	AAA	TAT	AAG	GAA	AAG	CAC	AAA	CCA	TTG	GGT	TCA	ATG	GAT	TGG	AAA	288
Pro	Lys	Tyr	Lys	Glu	Lys	His	Lys	Pro	Leu	Gly	Ser	Met	Asp	Trp	Lys	
				65					70					75		
AAA	CTG	CAA	AGA	GGA	GAA	CCA	AAT	AGT	TTT	AGT	GAG	AGG	GAT	GAA	TTG	336
Lys	Leu	Gln	Arg	Gly	Glu	Pro	Asn	Ser	Phe	Ser	Glu	Arg	Asp	Glu	Leu	
			80					85					90			
GAA	AAA	AAA	CGG	GGT	AGT	TCT	GAA	CTT	ATT	GAA	TCA	AAA	TGG	GAA	GAT	384
Glu	Lys	Lys	Arg	Gly	Ser	Ser	Glu	Leu	Ile	Glu	Ser	Lys	Trp	Glu	Asp	
		95					100					105				
GGG	CAA	AGT	CGT	GTA	GTT	GGT	TAT	ACA	AAT	TTC	ACT	TAT	GTC	CGT	TCG	432
Gly	Gln	Ser	Arg	Val	Val	Gly	Tyr	Thr	Asn	Phe	Thr	Tyr	Val	Arg	Ser	
	110					115					120					
GGA	TAT	GTT	TAC	CTT	AAT	AAA	AAT	AAT	ATT	GAT	ATT	AAG	AAT	AAT	ATA	480
Gly	Tyr	Val	Tyr	Leu	Asn	Lys	Asn	Asn	Ile	Asp	Ile	Lys	Asn	Asn	Ile	
125					130					135					140	
GTT	CTT	TTT	GGA	CCT	GAC	GGA	TAT	CTT	TAC	TAT	AAA	GGG	AAA	GAA	CCT	528
Val	Leu	Phe	Gly	Pro	Asp	Gly	Tyr	Leu	Tyr	Tyr	Lys	Gly	Lys	Glu	Pro	
				145					150					155		
TCC	AAG	GAG	CTG	CCA	TCG	GAA	AAG	ATA	ACT	TAT	AAA	GGT	ACT	TGG	GAT	576
Ser	Lys	Glu	Leu	Pro	Ser	Glu	Lys	Ile	Thr	Tyr	Lys	Gly	Thr	Trp	Asp	
			160					165					170			
TAT	GTT	ACT	GAT	GCT	ATG	GAA	AAA	CAA	AGG	TTT	GAA	GGA	TTG	GGT	AGT	624
Tyr	Val	Thr	Asp	Ala	Met	Glu	Lys	Gln	Arg	Phe	Glu	Gly	Leu	Gly	Ser	
		175					180					185				
GCA	GCA	GGA	GGA	GAT	AAA	TCG	GGG	GCG	TTG	TCT	GCA	TTA	GAA	GAA	GGG	672
Ala	Ala	Gly	Gly	Asp	Lys	Ser	Gly	Ala	Leu	Ser	Ala	Leu	Glu	Glu	Gly	
	190					195					200					
GTA	TTG	CGT	AAT	CAG	GCA	GAG	GCA	TCA	TCC	GGT	CAT	ACC	GAT	TTT	GGT	720
Val	Leu	Arg	Asn	Gln	Ala	Glu	Ala	Ser	Ser	Gly	His	Thr	Asp	Phe	Gly	
205				210						215					220	
ATG	ACT	AGT	GAG	TTT	GAG	GTT	GAT	TTT	TCT	GAT	AAA	ACA	ATA	AAG	GGC	768
Met	Thr	Ser	Glu	Phe	Glu	Val	Asp	Phe	Ser	Asp	Lys	Thr	Ile	Lys	Gly	
				225					230					235		
ACA	CTT	TAT	CGT	AAC	AAC	CGT	ATT	ACT	CAA	AAT	AAT	AGT	GAA	AAC	AAA	816
Thr	Leu	Tyr	Arg	Asn	Asn	Arg	Ile	Thr	Gln	Asn	Asn	Ser	Glu	Asn	Lys	
			240					245					250			
CAA	ATA	AAA	ACT	ACG	CGT	TAC	ACC	ATT	CAA	GCA	ACT	CTT	CAC	GGC	AAC	864
Gln	Ile	Lys	Thr	Thr	Arg	Tyr	Thr	Ile	Gln	Ala	Thr	Leu	His	Gly	Asn	
		255					260					265				

6. cont.

CGT	TTC	AAA	GGT	AAG	GCG	TTG	GCG	GCA	GAT	AAA	GGT	GCA	ACA	AAT	GGA	912
Arg	Phe	Lys	Gly	Lys	Ala	Leu	Ala	Ala	Asp	Lys	Gly	Ala	Thr	Asn	Gly	
270						275					280					
AGT	CAT	CCC	TTT	ATT	TCC	GAC	TCC	GAC	AGT	TTG	GAA	GGC	GGA	TTT	TAC	960
Ser	His	Pro	Phe	Ile	Ser	Asp	Ser	Asp	Ser	Leu	Glu	Gly	Gly	Phe	Tyr	
285					290					295					300	
GGG	CCG	AAA	GGC	GAG	GAA	CTT	GCC	GGT	AAA	TTC	TTG	AGC	AAC	GAC	AAC	1008
Gly	Pro	Lys	Gly	Glu	Glu	Leu	Ala	Gly	Lys	Phe	Leu	Ser	Asn	Asp	Asn	
				305					310					315		
AAA	GTT	GCA	GCG	GTG	TTT	GGT	GCG	AAG	CAG	AAA	GAT	AAG	AAG	GAT	GGG	1056
Lys	Val	Ala	Ala	Val	Phe	Gly	Ala	Lys	Gln	Lys	Asp	Lys	Lys	Asp	Gly	
				320				325						330		
GAA	AAC	GCG	GCA	GGG	CCT	GCA	ACG	GAA	ACC	GTG	ATA	GAT	GCA	TAC	CGT	1104
Glu	Asn	Ala	Ala	Gly	Pro	Ala	Thr	Glu	Thr	Val	Ile	Asp	Ala	Tyr	Arg	
				335				340				345				
ATT	ACC	GGC	GAG	GAG	TTT	AAG	AAA	GAG	CAA	ATA	GAC	AGT	TTT	GGA	GAT	1152
Ile	Thr	Gly	Glu	Glu	Phe	Lys	Lys	Glu	Gln	Ile	Asp	Ser	Phe	Gly	Asp	
						355					360					
GTG	AAA	AAG	CTG	CTG	GTT	GAC	GGA	GTG	GAG	CTT	TCA	CTG	CTG	CCG	TCT	1200
Val	Lys	Lys	Leu	Leu	Val	Asp	Gly	Val	Glu	Leu	Ser	Leu	Leu	Pro	Ser	
					370					375					380	
GAG	GGC	AAT	AAG	GCG	GCA	TTT	CAG	CAC	GAG	ATT	GAG	CAA	AAC	GGC	GTG	1248
Glu	Gly	Asn	Lys	Ala	Ala	Phe	Gln	His	Glu	Ile	Glu	Gln	Asn	Gly	Val	
				385					390					395		
AAG	GCA	ACG	GTG	TGT	TGT	TCC	AAC	TTG	GAT	TAC	ATG	AGT	TTT	GGG	AAG	1296
Lys	Ala	Thr	Val	Cys	Cys	Ser	Asn	Leu	Asp	Tyr	Met	Ser	Phe	Gly	Lys	
				400				405						410		
CTG	TCA	AAA	GAA	AAT	AAA	GAC	GAT	ATG	TTC	CTG	CAA	GGT	GTC	CGC	ACT	1344
Leu	Ser	Lys	Glu	Asn	Lys	Asp	Asp	Met	Phe	Leu	Gln	Gly	Val	Arg	Thr	
				415				420					425			
CCA	GTA	TCC	GAT	GTG	GCG	GCA	AGG	ACG	GAG	GCA	AAC	GCC	AAA	TAT	CGC	1392
Pro	Val	Ser	Asp	Val	Ala	Ala	Arg	Thr	Glu	Ala	Asn	Ala	Lys	Tyr	Arg	
						435						440				
GGT	ACT	TGG	TAC	GGA	TAT	ATT	GCC	AAC	GGC	ACA	AGC	TGG	AGC	GGC	GAA	1440
Gly	Thr	Trp	Tyr	Gly	Tyr	Ile	Ala	Asn	Gly	Thr	Ser	Trp	Ser	Gly	Glu	
					450					455					460	
GCC	TCC	AAT	CAG	GAA	GGT	GGT	AAT	AGG	GCA	GAG	TTT	GAC	GTG	GAT	TTT	1488
Ala	Ser	Asn	Gln	Glu	Gly	Gly	Asn	Arg	Ala	Glu	Phe	Asp	Val	Asp	Phe	
				465					470					475		

6 cont.

TCC ACT AAA AAA ATC AGT GGC ACA CTG ACG GCA AAA GAC CGT ACG TCT	1536
Ser Thr Lys Lys Ile Ser Gly Thr Leu Thr Ala Lys Asp Arg Thr Ser	
480 485 490	
CCT GCG TTT ACT ATT ACT GCC ATG ATT AAG GAC AAC GGT TTT TCA GGT	1584
Pro Ala Phe Thr Ile Thr Ala Met Ile Lys Asp Asn Gly Phe Ser Gly	
495 500 505	
GTG GCG AAA ACC GGT GAA AAC GGC TTT GCG CTG GAT CCG CAA AAT ACC	1632
Val Ala Lys Thr Gly Glu Asn Gly Phe Ala Leu Asp Pro Gln Asn Thr	
510 515 520	
GGA AAT TCC CAC TAT ACG CAT ATT GAA GCC ACT GTA TCC GGC GGT TTC	1680
Gly Asn Ser His Tyr Thr His Ile Glu Ala Thr Val Ser Gly Gly Phe	
525 530 535 540	
TAC GGC AAA AAC GCC ATC GAG ATG GGC GGA TCG TTC TCA TTT CCG GGA	1728
Tyr Gly Lys Asn Ala Ile Glu Met Gly Gly Ser Phe Ser Phe Pro Gly	
545 550 555	
AAT GCA CCA GAG GGA AAA CAA GAA AAA GCA TCG GTG GTA TTC GGT GCG	1776
Asn Ala Pro Glu Gly Lys Gln Glu Lys Ala Ser Val Val Phe Gly Ala	
560 565 570	
AAA CGC CAA CAG CTT GTG CAA TAAGCACGGC T	1808
Lys Arg Gln Gln Leu Val Gln	
575	

*b cont.*  
(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 599 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Asn Asn Pro Leu Val Asn Gln Ala Ala Met Val Leu Pro Val Phe	
-20 -15 -10 -5	
Leu Leu Ser Ala Cys Leu Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser	
1 5 10	
Val Glu Thr Val Gln Asp Met His Ser Lys Pro Lys Tyr Glu Asp Glu	
15 20 25	
Lys Ser Gln Pro Glu Ser Gln Gln Asp Val Ser Glu Asn Ser Gly Ala	
30 35 40	
Ala Tyr Gly Phe Ala Val Lys Leu Pro Arg Arg Asn Ala His Phe Asn	
45 50 55 60	

Pro Lys Tyr Lys Glu Lys His Lys Pro Leu Gly Ser Met Asp Trp Lys  
 65 70 75  
 Lys Leu Gln Arg Gly Glu Pro Asn Ser Phe Ser Glu Arg Asp Glu Leu  
 80 85 90  
 Glu Lys Lys Arg Gly Ser Ser Glu Leu Ile Glu Ser Lys Trp Glu Asp  
 95 100 105  
 Gly Gln Ser Arg Val Val Gly Tyr Thr Asn Phe Thr Tyr Val Arg Ser  
 110 115 120  
 Gly Tyr Val Tyr Leu Asn Lys Asn Asn Ile Asp Ile Lys Asn Asn Ile  
 125 130 135 140  
 Val Leu Phe Gly Pro Asp Gly Tyr Leu Tyr Tyr Lys Gly Lys Glu Pro  
 145 150 155  
 Ser Lys Glu Leu Pro Ser Glu Lys Ile Thr Tyr Lys Gly Thr Trp Asp  
 160 165 170  
 Tyr Val Thr Asp Ala Met Glu Lys Gln Arg Phe Glu Gly Leu Gly Ser  
 175 180 185  
 Ala Ala Gly Gly Asp Lys Ser Gly Ala Leu Ser Ala Leu Glu Glu Gly  
 190 195 200  
 Val Leu Arg Asn Gln Ala Glu Ala Ser Ser Gly His Thr Asp Phe Gly  
 205 210 215 220  
 Met Thr Ser Glu Phe Glu Val Asp Phe Ser Asp Lys Thr Ile Lys Gly  
 225 230 235  
 Thr Leu Tyr Arg Asn Asn Arg Ile Thr Gln Asn Asn Ser Glu Asn Lys  
 240 245 250  
 Gln Ile Lys Thr Thr Arg Tyr Thr Ile Gln Ala Thr Leu His Gly Asn  
 255 260 265  
 Arg Phe Lys Gly Lys Ala Leu Ala Ala Asp Lys Gly Ala Thr Asn Gly  
 270 275 280  
 Ser His Pro Phe Ile Ser Asp Ser Asp Ser Leu Glu Gly Gly Phe Tyr  
 285 290 295 300  
 Gly Pro Lys Gly Glu Glu Leu Ala Gly Lys Phe Leu Ser Asn Asp Asn  
 305 310 315  
 Lys Val Ala Ala Val Phe Gly Ala Lys Gln Lys Asp Lys Lys Asp Gly  
 320 325 330  
 Glu Asn Ala Ala Gly Pro Ala Thr Glu Thr Val Ile Asp Ala Tyr Arg  
 335 340 345

Ile Thr Gly Glu Glu Phe Lys Lys Glu Gln Ile Asp Ser Phe Gly Asp  
 350 355 360  
 Val Lys Lys Leu Leu Val Asp Gly Val Glu Leu Ser Leu Leu Pro Ser  
 365 370 375 380  
 Glu Gly Asn Lys Ala Ala Phe Gln His Glu Ile Glu Gln Asn Gly Val  
 385 390 395  
 Lys Ala Thr Val Cys Cys Ser Asn Leu Asp Tyr Met Ser Phe Gly Lys  
 400 405 410  
 Leu Ser Lys Glu Asn Lys Asp Asp Met Phe Leu Gln Gly Val Arg Thr  
 415 420 425  
 Pro Val Ser Asp Val Ala Ala Arg Thr Glu Ala Asn Ala Lys Tyr Arg  
 430 435 440  
 Gly Thr Trp Tyr Gly Tyr Ile Ala Asn Gly Thr Ser Trp Ser Gly Glu  
 445 450 455 460  
 Ala Ser Asn Gln Glu Gly Gly Asn Arg Ala Glu Phe Asp Val Asp Phe  
 465 470 475  
 Ser Thr Lys Lys Ile Ser Gly Thr Leu Thr Ala Lys Asp Arg Thr Ser  
 480 485 490  
 Pro Ala Phe Thr Ile Thr Ala Met Ile Lys Asp Asn Gly Phe Ser Gly  
 495 500 505  
 Val Ala Lys Thr Gly Glu Asn Gly Phe Ala Leu Asp Pro Gln Asn Thr  
 510 515 520  
 Gly Asn Ser His Tyr Thr His Ile Glu Ala Thr Val Ser Gly Gly Phe  
 525 530 535 540  
 Tyr Gly Lys Asn Ala Ile Glu Met Gly Gly Ser Phe Ser Phe Pro Gly  
 545 550 555  
 Asn Ala Pro Glu Gly Lys Gln Glu Lys Ala Ser Val Val Phe Gly Ala  
 560 565 570  
 Lys Arg Gln Gln Leu Val Gln  
 575

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2255 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: N. meningitidis  
(B) STRAIN: M978

(ix) FEATURE:

(A) NAME/KEY: mat\_peptide  
(B) LOCATION: 1..2115

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 1..2115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TGT	CTG	GGT	GGC	GGC	GGC	ACG	TTC	GAT	CTT	GAT	TCT	GTC	GAT	ACC	GAA	48
Cys	Leu	Gly	Gly	Gly	Gly	Thr	Phe	Asp	Leu	Asp	Ser	Val	Asp	Thr	Glu	
1				5				10						15		
GCC	CCG	CGT	CCC	GCC	CCA	AAA	TAT	CAA	GAT	GTT	TCT	TCC	GAA	AAA	CCG	96
Ala	Pro	Arg	Pro	Ala	Pro	Lys	Tyr	Gln	Asp	Val	Ser	Ser	Glu	Lys	Pro	
			20					25					30			
CAA	GCC	CAA	AAA	GAC	CAA	GGC	GGA	TAC	GGT	TTT	GCA	ATG	CGC	CTC	AAG	144
Gln	Ala	Gln	Lys	Asp	Gln	Gly	Gly	Tyr	Gly	Phe	Ala	Met	Arg	Leu	Lys	
			35				40					45				
CGG	CGG	AAT	TGG	CAT	CCG	CAG	GCA	AAT	CCT	AAA	GAA	GAT	GAG	ATA	AAA	192
Arg	Arg	Asn	Trp	His	Pro	Gln	Ala	Asn	Pro	Lys	Glu	Asp	Glu	Ile	Lys	
B. y. cont.	50					55					60					
CTT	TCT	GAA	AAT	GAT	TGG	GAG	GCG	ACA	GGA	TTG	CCA	GGC	AAT	CCC	AAA	240
Leu	Ser	Glu	Asn	Asp	Trp	Glu	Ala	Thr	Gly	Leu	Pro	Gly	Asn	Pro	Lys	
65					70				75						80	
AAC	TTA	CCT	GAG	CGA	CAG	AAA	TCG	GTT	ATT	GAA	AAA	GTA	AAA	ACA	GGC	288
Asn	Leu	Pro	Glu	Arg	Gln	Lys	Ser	Val	Ile	Glu	Lys	Val	Lys	Thr	Gly	
				85				90						95		
AGC	GAC	AGC	AAT	ATT	TAT	TCT	TCC	CCC	TAT	CTC	ACG	CAA	TCA	AAC	CAT	336
Ser	Asp	Ser	Asn	Ile	Tyr	Ser	Ser	Pro	Tyr	Leu	Thr	Gln	Ser	Asn	His	
			100					105					110			
CAA	AAC	GGC	AGT	GCA	AAC	CAA	CCA	AAA	AAT	GAA	GTA	AAA	GAT	TAT	AAA	384
Gln	Asn	Gly	Ser	Ala	Asn	Gln	Pro	Lys	Asn	Glu	Val	Lys	Asp	Tyr	Lys	
		115					120					125				
GAG	TTC	AAA	TAT	GTT	TAT	TCC	GGT	TGG	TTT	TAC	AAA	CAC	GCT	AAA	CTC	432
Glu	Phe	Lys	Tyr	Val	Tyr	Ser	Gly	Trp	Phe	Tyr	Lys	His	Ala	Lys	Leu	
	130					135					140					
GAA	ATC	ATA	AAA	GAA	AAC	AAC	TTA	ATT	AAG	GGT	GCA	AAG	AGC	GGC	GAC	480
Glu	Ile	Ile	Lys	Glu	Asn	Asn	Leu	Ile	Lys	Gly	Ala	Lys	Ser	Gly	Asp	
145					150					155					160	

GAC	GGT	TAT	ATC	TTT	TAT	CAC	GGT	GAA	AAA	CCT	TCC	CGA	CAA	CTT	CCC	528
Asp	Gly	Tyr	Ile	Phe	Tyr	His	Gly	Glu	Lys	Pro	Ser	Arg	Gln	Leu	Pro	
				165					170						175	
GTT	TCT	GGA	GAA	GTT	ACC	TAC	AAA	GGC	GTA	TGG	CAT	TTT	GTA	ACC	GAT	576
Val	Ser	Gly	Glu	Val	Thr	Tyr	Lys	Gly	Val	Trp	His	Phe	Val	Thr	Asp	
			180					185					190			
ACG	AAA	CAG	GGA	CAA	AAA	TTT	AAC	GAT	ATT	CTT	GGA	ACC	TCA	AAA	AAA	624
Thr	Lys	Gln	Gly	Gln	Lys	Phe	Asn	Asp	Ile	Leu	Gly	Thr	Ser	Lys	Lys	
		195					200					205				
CAA	GGC	GAC	AGG	TAT	AGC	GGA	TTT	CCG	GGT	GAT	GAC	GGC	GAA	GAA	TAT	672
Gln	Gly	Asp	Arg	Tyr	Ser	Gly	Phe	Pro	Gly	Asp	Asp	Gly	Glu	Glu	Tyr	
	210					215					220					
TCC	AAT	AAA	AAT	GAA	GCG	ACT	TTA	CAA	GGC	AGT	CAA	GAG	GGT	TAT	GGT	720
Ser	Asn	Lys	Asn	Glu	Ala	Thr	Leu	Gln	Gly	Ser	Gln	Glu	Gly	Tyr	Gly	
225				230						235					240	
TTT	ACC	TCA	AAT	TTA	AAA	GTG	GAT	TTC	AAT	AAG	AAA	AAA	TTG	ACG	GGT	768
Phe	Thr	Ser	Asn	Leu	Lys	Val	Asp	Phe	Asn	Lys	Lys	Lys	Leu	Thr	Gly	
			245						250					255		
GAA	TTG	ATA	CGC	AAT	AAT	AGA	GTT	ACA	AAC	GCT	ACT	GCT	AAC	GAT	AAA	816
(Glu	Leu	Ile	Arg	Asn	Asn	Arg	Val	Thr	Asn	Ala	Thr	Ala	Asn	Asp	Lys	
cont.			260					265					270			
TAC	ACC	ACC	CAA	TAT	TAC	AGC	CTT	GAG	GCT	CAA	GTA	ACA	GGC	AAC	CGC	864
Tyr	Thr	Thr	Gln	Tyr	Tyr	Ser	Leu	Glu	Ala	Gln	Val	Thr	Gly	Asn	Arg	
		275					280					285				
TTC	AAC	GGC	AAG	GCA	ACG	GCA	ACC	GAC	AAA	CCT	GGC	ACT	GGA	GAA	ACC	912
Phe	Asn	Gly	Lys	Ala	Thr	Ala	Thr	Asp	Lys	Pro	Gly	Thr	Gly	Glu	Thr	
	290					295					300					
AAA	CAA	CAT	CCC	TTT	GTT	TCC	GAC	TCG	TCT	TCT	TTG	AGC	GGC	GGC	TTT	960
Lys	Gln	His	Pro	Phe	Val	Ser	Asp	Ser	Ser	Ser	Leu	Ser	Gly	Gly	Phe	
305				310						315					320	
TTC	GGC	CCG	AAG	GGT	GAG	GAA	TTG	GGT	TTC	CGC	TTT	TTG	AGC	AAC	GAT	1008
Phe	Gly	Pro	Lys	Gly	Glu	Glu	Leu	Gly	Phe	Arg	Phe	Leu	Ser	Asn	Asp	
				325					330					335		
CAA	AAA	GTT	GCC	GTT	GTC	GGC	AGC	GCG	AAA	ACC	CAA	GAC	AAA	GCC	GCA	1056
Gln	Lys	Val	Ala	Val	Val	Gly	Ser	Ala	Lys	Thr	Gln	Asp	Lys	Ala	Ala	
			340					345					350			
AAT	GGC	AAT	ACT	GCG	GCG	GCT	TCA	GGC	GGC	ACA	GAT	GCG	GCA	GCA	TCA	1104
Asn	Gly	Asn	Thr	Ala	Ala	Ala	Ser	Gly	Gly	Thr	Asp	Ala	Ala	Ala	Ser	
		355					360					365				



AAC Asn 370	GGT Gly 370	GCG Ala 370	GCA Ala 370	GGC Gly 370	ACG Thr 375	TCG Ser 375	TCT Ser 375	GAA Glu 375	AAC Asn 375	AGT Ser 375	AAG Lys 380	CTG Leu 380	ACC Thr 380	ACG Thr 380	GTT Val 380	1152
TTG Leu 385	GAT Asp 385	GCG Ala 385	GTT Val 385	GAA Glu 390	TTG Leu 390	ACA Thr 390	CTA Leu 390	AAC Asn 390	GAC Asp 395	AAG Lys 395	AAA Lys 395	ATC Ile 395	AAA Lys 395	AAT Asn 400	CTC Leu 400	1200
GAC Asp 405	AAC Asn 405	TTC Phe 405	AGC Ser 405	AAT Asn 405	GCC Ala 410	GCC Ala 410	CAA Gln 410	CTG Leu 410	GTT Val 410	GTC Val 410	GAC Asp 415	GGC Gly 415	ATT Ile 415	ATG Met 415	ATT Ile 415	1248
CCG Pro 420	CTC Leu 420	CTG Leu 420	CCC Pro 420	GAG Glu 425	ACT Thr 425	TCC Ser 425	GAA Glu 425	AGT Ser 425	GGG Gly 425	AGC Ser 425	AAT Asn 430	CAG Gln 430	GCA Ala 430	GAT Asp 430	AAA Lys 430	1296
GGT Gly 435	AAA Lys 435	AAA Lys 435	GGT Gly 435	AAA Lys 440	AAC Asn 440	GGT Gly 440	AAA Lys 440	AAC Asn 440	GGC Gly 445	GGA Gly 445	ACA Thr 445	GAC Asp 445	TTT Phe 445	ACC Thr 445	TAC Tyr 445	1344
AAA Lys 450	ACA Thr 450	ACC Thr 450	TAC Tyr 450	ACG Thr 455	CCG Pro 455	AAA Lys 455	AAC Asn 455	GAT Asp 455	GAC Asp 460	AAA Lys 460	GAT Asp 460	ACC Thr 460	AAA Lys 460	GCC Ala 460	CAA Gln 460	1392
ACA Thr 465	GGT Gly 465	GCG Ala 465	GCA Ala 465	GGC Gly 470	TCT Ser 470	AGC Ser 470	GGC Gly 470	GCA Ala 470	CAA Gln 475	ACC Thr 475	GAT Asp 475	TTG Leu 475	GGT Gly 475	AAG Lys 475	GCG Ala 480	1440
GAC Asp 485	GTT Val 485	AAC Asn 485	GGC Gly 485	GGT Gly 485	AAG Lys 485	GCA Ala 485	GAA Glu 485	ACA Thr 485	AAA Lys 490	ACC Thr 490	TAT Tyr 490	GAA Glu 495	GTC Val 495	GAA Glu 495	GTC Val 495	1488
TGC Cys 500	TGT Cys 500	TCC Ser 500	AAC Asn 500	CTC Leu 500	AAT Asn 500	TAT Tyr 500	CTG Leu 505	AAA Lys 505	TAC Tyr 505	GGA Gly 505	ATG Met 505	TTG Leu 510	ACG Thr 510	CGT Arg 510	AAA Lys 510	1536
AAC Asn 515	AGC Ser 515	AAG Lys 515	TCC Ser 515	GCG Ala 515	ATG Met 515	CAG Gln 515	GCA Ala 520	GGA Gly 520	GGA Gly 520	AAC Asn 520	AGT Ser 525	AGT Ser 525	CAA Gln 525	GCT Ala 525	GAT Asp 525	1584
GCT Ala 530	AAA Lys 530	ACG Thr 530	GAA Glu 530	CAA Gln 535	GTT Val 535	GAA Glu 535	CAA Gln 535	AGT Ser 535	ATG Met 535	TTC Phe 540	CTC Leu 540	CAA Gln 540	GGC Gly 540	GAG Glu 540	CGT Arg 540	1632
ACC Thr 545	GAT Asp 545	GAA Glu 545	AAA Lys 545	GAG Glu 550	ATT Ile 550	CCA Pro 550	AAC Asn 550	GAC Asp 550	CAA Gln 555	AAC Asn 555	GTC Val 555	GTT Val 555	TAT Tyr 555	CGG Arg 555	GGG Gly 560	1680
TCT Ser 565	TGG Trp 565	TAC Tyr 565	GGG Gly 565	CAT His 565	ATT Ile 565	GCC Ala 565	AGC Ser 565	AGC Ser 565	ACA Thr 570	AGC Ser 570	TGG Trp 570	AGC Ser 570	GGC Gly 570	AAT Asn 575	GCT Ala 575	1728

TCC AAT GCA ACG AGT GGC AAC AGG GCG GAA TTT ACT GTG AAT TTC GAT	1776
Ser Asn Ala Thr Ser Gly Asn Arg Ala Glu Phe Thr Val Asn Phe Asp	
580 585 590	
ACG AAA AAA ATT AAC GGC ACG TTA ACC GCT GAA AAC AGG CAG GAG GCA	1824
Thr Lys Lys Ile Asn Gly Thr Leu Thr Ala Glu Asn Arg Gln Glu Ala	
595 600 605	
ACC TTT ACC ATT GAT GGT AAG ATT GAG GGC AAC GGT TTT TCC GGT ACC	1872
Thr Phe Thr Ile Asp Gly Lys Ile Glu Gly Asn Gly Phe Ser Gly Thr	
610 615 620	
GCA AAA ACT GCT GAC TTA GGT TTT GAT CTC GAT CAA AGC AAT ACC ACC	1920
Ala Lys Thr Ala Asp Leu Gly Phe Asp Leu Asp Gln Ser Asn Thr Thr	
625 630 635 640	
GGC ACG CCT AAG GCA TAT ATC ACA GAT GCC AAG GTG CAG GGC GGT TTT	1968
Gly Thr Pro Lys Ala Tyr Ile Thr Asp Ala Lys Val Gln Gly Gly Phe	
645 650 655	
TAC GGG CCT AAA GCC GAA GAG TTG GGC GGA TGG TTT GCC TAT CCG GGC	2016
Tyr Gly Pro Lys Ala Glu Glu Leu Gly Gly Trp Phe Ala Tyr Pro Gly	
660 665 670	
GAT AAA CAA ACG GAA AAG GCA ACG GTT GCA TCC GGC GAT GGA AAT TCA	2064
Asp Lys Gln Thr Glu Lys Ala Thr Val Ala Ser Gly Asp Gly Asn Ser	
675 680 685	
GCA AGC AGC GCG ACC GTG GTA TTC GGT GCG AAA CGC CAA CAG CCT GTG	2112
Ala Ser Ser Ala Thr Val Val Phe Gly Ala Lys Arg Gln Gln Pro Val	
690 695 700	
CAA TAACTAAATG AAGTTGTCTG GGTGGCGGCG GCACGTTCGA TCTTGATTCT	2165
Gln	
705	
GTCGATACCG AAGCCCCGCG TCCCGCCCCA AAATATCAAG ATGTTTCTTC CGAAAAACCG	2225
CAAGCCCAAA AAGACCAAGG CGGATACGGT	2255

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 705 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Cys	Leu	Gly	Gly	Gly	Gly	Thr	Phe	Asp	Leu	Asp	Ser	Val	Asp	Thr	Glu
1				5					10					15	

Ala Pro Arg Pro Ala Pro Lys Tyr Gln Asp Val Ser Ser Glu Lys Pro  
 20 25 30  
 Gln Ala Gln Lys Asp Gln Gly Gly Tyr Gly Phe Ala Met Arg Leu Lys  
 35 40 45  
 Arg Arg Asn Trp His Pro Gln Ala Asn Pro Lys Glu Asp Glu Ile Lys  
 50 55 60  
 Leu Ser Glu Asn Asp Trp Glu Ala Thr Gly Leu Pro Gly Asn Pro Lys  
 65 70 75 80  
 Asn Leu Pro Glu Arg Gln Lys Ser Val Ile Glu Lys Val Lys Thr Gly  
 85 90 95  
 Ser Asp Ser Asn Ile Tyr Ser Ser Pro Tyr Leu Thr Gln Ser Asn His  
 100 105 110  
 Gln Asn Gly Ser Ala Asn Gln Pro Lys Asn Glu Val Lys Asp Tyr Lys  
 115 120 125  
 Glu Phe Lys Tyr Val Tyr Ser Gly Trp Phe Tyr Lys His Ala Lys Leu  
 130 135 140  
 Glu Ile Ile Lys Glu Asn Asn Leu Ile Lys Gly Ala Lys Ser Gly Asp  
 145 150 155 160  
 Asp Gly Tyr Ile Phe Tyr His Gly Glu Lys Pro Ser Arg Gln Leu Pro  
 165 170 175  
 Val Ser Gly Glu Val Thr Tyr Lys Gly Val Trp His Phe Val Thr Asp  
 180 185 190  
 Thr Lys Gln Gly Gln Lys Phe Asn Asp Ile Leu Gly Thr Ser Lys Lys  
 195 200 205  
 Gln Gly Asp Arg Tyr Ser Gly Phe Pro Gly Asp Asp Gly Glu Glu Tyr  
 210 215 220  
 Ser Asn Lys Asn Glu Ala Thr Leu Gln Gly Ser Gln Glu Gly Tyr Gly  
 225 230 235 240  
 Phe Thr Ser Asn Leu Lys Val Asp Phe Asn Lys Lys Lys Leu Thr Gly  
 245 250 255  
 Glu Leu Ile Arg Asn Asn Arg Val Thr Asn Ala Thr Ala Asn Asp Lys  
 260 265 270  
 Tyr Thr Thr Gln Tyr Tyr Ser Leu Glu Ala Gln Val Thr Gly Asn Arg  
 275 280 285  
 Phe Asn Gly Lys Ala Thr Ala Thr Asp Lys Pro Gly Thr Gly Glu Thr  
 290 295 300

Lys Gln His Pro Phe Val Ser Asp Ser Ser Ser Leu Ser Gly Gly Phe  
 305 310 315 320  
 Phe Gly Pro Lys Gly Glu Glu Leu Gly Phe Arg Phe Leu Ser Asn Asp  
 325 330 335  
 Gln Lys Val Ala Val Val Gly Ser Ala Lys Thr Gln Asp Lys Ala Ala  
 340 345 350  
 Asn Gly Asn Thr Ala Ala Ala Ser Gly Gly Thr Asp Ala Ala Ala Ser  
 355 360 365  
 Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn Ser Lys Leu Thr Thr Val  
 370 375 380  
 Leu Asp Ala Val Glu Leu Thr Leu Asn Asp Lys Lys Ile Lys Asn Leu  
 385 390 395 400  
 Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp Gly Ile Met Ile  
 405 410 415  
 Pro Leu Leu Pro Glu Thr Ser Glu Ser Gly Ser Asn Gln Ala Asp Lys  
 420 425 430  
 Gly Lys Lys Gly Lys Asn Gly Lys Asn Gly Gly Thr Asp Phe Thr Tyr  
 435 440 445  
 Lys Thr Thr Tyr Thr Pro Lys Asn Asp Asp Lys Asp Thr Lys Ala Gln  
 450 455 460  
 Thr Gly Ala Ala Gly Ser Ser Gly Ala Gln Thr Asp Leu Gly Lys Ala  
 465 470 475 480  
 Asp Val Asn Gly Gly Lys Ala Glu Thr Lys Thr Tyr Glu Val Glu Val  
 485 490 495  
 Cys Cys Ser Asn Leu Asn Tyr Leu Lys Tyr Gly Met Leu Thr Arg Lys  
 500 505 510  
 Asn Ser Lys Ser Ala Met Gln Ala Gly Gly Asn Ser Ser Gln Ala Asp  
 515 520 525  
 Ala Lys Thr Glu Gln Val Glu Gln Ser Met Phe Leu Gln Gly Glu Arg  
 530 535 540  
 Thr Asp Glu Lys Glu Ile Pro Asn Asp Gln Asn Val Val Tyr Arg Gly  
 545 550 555 560  
 Ser Trp Tyr Gly His Ile Ala Ser Ser Thr Ser Trp Ser Gly Asn Ala  
 565 570 575  
 Ser Asn Ala Thr Ser Gly Asn Arg Ala Glu Phe Thr Val Asn Phe Asp  
 580 585 590

Thr Lys Lys Ile Asn Gly Thr Leu Thr Ala Glu Asn Arg Gln Glu Ala  
 595 600 605  
 Thr Phe Thr Ile Asp Gly Lys Ile Glu Gly Asn Gly Phe Ser Gly Thr  
 610 615 620  
 Ala Lys Thr Ala Asp Leu Gly Phe Asp Leu Asp Gln Ser Asn Thr Thr  
 625 630 635 640  
 Gly Thr Pro Lys Ala Tyr Ile Thr Asp Ala Lys Val Gln Gly Gly Phe  
 645 650 655  
 Tyr Gly Pro Lys Ala Glu Glu Leu Gly Gly Trp Phe Ala Tyr Pro Gly  
 660 665 670  
 Asp Lys Gln Thr Glu Lys Ala Thr Val Ala Ser Gly Asp Gly Asn Ser  
 675 680 685  
 Ala Ser Ser Ala Thr Val Val Phe Gly Ala Lys Arg Gln Gln Pro Val  
 690 695 700  
 Gln  
 705

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2114 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *N. meningitidis*  
 (B) STRAIN: 6940

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide  
 (B) LOCATION: 1..2079

(ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 1..2079

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TGT TTG GGT GGC GGC GGC ACG TTC GAT CTT GAT TCT GTC GAT ACC GAA  
 Cys Leu Gly Gly Gly Gly Thr Phe Asp Leu Asp Ser Val Asp Thr Glu  
 1 5 10 15

GCC	CCG	CGT	CCC	GAC	CCA	AAG	TAT	CAA	GAT	GTT	TCT	TCC	GAA	AAA	CCG	96
Ala	Pro	Arg	Pro	Asp	Pro	Lys	Tyr	Gln	Asp	Val	Ser	Ser	Glu	Lys	Pro	
			20					25					30			
CAA	GCC	CAA	AAA	GAC	CAA	GGC	GGA	TAC	GGT	TTT	GCG	ATG	AGG	TTG	AAA	144
Gln	Ala	Gln	Lys	Asp	Gln	Gly	Gly	Tyr	Gly	Phe	Ala	Met	Arg	Leu	Lys	
		35				40					45					
CGG	AGG	AAT	TGG	TAT	TCC	GCA	GCA	AAA	GAA	GAC	GAG	GTT	AAA	CTG	AAC	192
Arg.	Arg	Asn	Trp	Tyr	Ser	Ala	Ala	Lys	Glu	Asp	Glu	Val	Lys	Leu	Asn	
	50					55					60					
GAG	AGT	GAT	TGG	GAG	ACG	ACA	GGA	TTG	CCG	ACA	GAA	CCC	AAG	AAA	CTG	240
Glu	Ser	Asp	Trp	Glu	Thr	Thr	Gly	Leu	Pro	Thr	Glu	Pro	Lys	Lys	Leu	
65					70					75					80	
CCA	TTA	AAA	CAA	GAA	TCC	GTC	ATT	TCA	AAA	GTA	CAA	GCA	AAC	AAT	GGC	288
Pro	Leu	Lys	Gln	Glu	Ser	Val	Ile	Ser	Lys	Val	Gln	Ala	Asn	Asn	Gly	
				85					90					95		
GAC	AAC	AAT	ATT	TAC	ACT	TCC	CCC	TAT	CTC	ACG	CAA	TCA	AAC	CAT	CAA	336
Asp	Asn	Asn	Ile	Tyr	Thr	Ser	Pro	Tyr	Leu	Thr	Gln	Ser	Asn	His	Gln	
			100					105					110			
AAT	AGC	AGC	ATT	AAT	GGC	GGT	GCA	AAC	CTG	CCA	AAA	AAC	GAA	GTA	ACA	384
Asn	Ser	Ser	Ile	Asn	Gly	Gly	Ala	Asn	Leu	Pro	Lys	Asn	Glu	Val	Thr	
		115				120						125				
AAT	TAT	AAA	GAT	TTC	AAA	TAT	GTT	TAT	TCC	GGC	TGG	TTT	TAT	AAA	CAT	432
Asn	Tyr	Lys	Asp	Phe	Lys	Tyr	Val	Tyr	Ser	Gly	Trp	Phe	Tyr	Lys	His	
	130					135					140					
GCT	AAA	AAC	GAA	ATC	ATA	AGA	GAA	AAC	AGC	TCA	ATT	AAG	GGT	GCA	AAG	480
Ala	Lys	Asn	Glu	Ile	Ile	Arg	Glu	Asn	Ser	Ser	Ile	Lys	Gly	Ala	Lys	
145					150					155					160	
AAC	GGC	GAC	GAC	GGC	TAT	ATC	TTT	TAT	CAC	GGC	AAA	GAA	CCT	TCC	CGA	528
Asn	Gly	Asp	Asp	Gly	Tyr	Ile	Phe	Tyr	His	Gly	Lys	Glu	Pro	Ser	Arg	
				165					170					175		
CAA	CTT	CCC	GCT	TCT	GGA	ACA	GTT	ACC	TAT	AAA	GGT	GTG	TGG	CAT	TTT	576
Gln	Leu	Pro	Ala	Ser	Gly	Thr	Val	Thr	Tyr	Lys	Gly	Val	Trp	His	Phe	
			180					185					190			
GCG	ACC	GAT	GTC	AAA	AAA	TCC	CAA	AAT	TTT	CGC	GAT	ATT	ATC	CAG	CCT	624
Ala	Thr	Asp	Val	Lys	Lys	Ser	Gln	Asn	Phe	Arg	Asp	Ile	Ile	Gln	Pro	
		195					200					205				
TCG	AAA	AAA	CAA	GGC	GAC	AGG	TAT	AGC	GGA	TTT	TCG	GGC	GAT	GAT	GAT	672
Ser	Lys	Lys	Gln	Gly	Asp	Arg	Tyr	Ser	Gly	Phe	Ser	Gly	Asp	Asp	Asp	
	210					215					220					

GAA Glu 225	CAA Gln	TAT Tyr	TCT Ser	AAT Asn	AAA Lys 230	AAC Asn	GAA Glu	TCC Ser	ATG Met	CTG Leu 235	AAA Lys	GAT Asp	GGT Gly	CAA Gln	GAG Glu 240	720
GGT Gly	TAT Tyr	GGT Gly	TTT Phe	ACC Thr 245	TCG Ser	AAT Asn	TTA Leu	GAA Glu	GTG Val 250	GAT Asp	TTC Phe	GGC Gly	AGT Ser	AAA Lys 255	AAA Lys	768
TTG Leu	ACG Thr	GGT Gly	AAA Lys 260	TTA Leu	ATA Ile	CGC Arg	AAT Asn	AAT Asn 265	AGA Arg	GTT Val	ACA Thr	AAC Asn	GCT Ala 270	CCT Pro	ACT Thr	816
AAC Asn	GAT Asp	AAA Lys 275	TAC Tyr	ACC Thr	ACC Thr	CAA Gln	TAC Tyr 280	TAC Tyr	AGC Ser	CTT Leu	GAT Asp	GCC Ala 285	CAA Gln	ATA Ile	ACA Thr	864
GGC Gly	AAC Asn 290	CGC Arg	TTC Phe	AAC Asn	GGT Gly	AAG Lys 295	GCG Ala	ATA Ile	CGG Arg	ACC Thr	GAC Asp 300	AAA Lys	CCC Pro	GAC Asp	ACT Thr	912
GGA Gly 305	GGA Gly	ACC Thr	AAA Lys	CTA Leu	CAT His 310	CCC Pro	TTT Phe	GTT Val	TCC Ser	GAC Asp 315	TCG Ser	TCT Ser	TCT Ser	TTG Leu	AGC Ser 320	960
GGC Gly	GGC Gly	TTT Phe	TTC Phe	GGT Gly 325	CCG Pro	AAG Lys	GGT Gly	GAG Glu	GAA Glu 330	TTG Leu	GGT Gly	TTC Phe	CGC Arg	TTT Phe 335	TTG Leu	1008
AGC Ser	GAC Asp	GAT Asp	AAA Lys 340	AAA Lys	GTT Val	GCG Ala	GTT Val	GTC Val 345	GGC Gly	AGC Ser	GCG Ala	AAA Lys	ACC Thr 350	AAA Lys	GAC Asp	1056
AAA Lys	ACG Thr	GAA Glu 355	AAT Asn	GGC Gly	GCG Ala	GTG Val	GCT Ala 360	TCA Ser	GGC Gly	GGC Gly	ACA Thr	GAT Asp 365	GCG Ala	GCA Ala	GCA Ala	1104
TCA Ser	AAC Asn 370	GGT Gly	GCG Ala	GCA Ala	GGC Gly	ACG Thr 375	TCG Ser	TCT Ser	GAA Glu	AAC Asn	AGT Ser 380	AAG Lys	CTG Leu	ACC Thr	ACG Thr	1152
GTT Val 385	TTG Leu	GAT Asp	GCG Ala	GTC Val	GAG Glu 390	CTG Leu	AAA Lys	TTG Leu	GGC Gly	GAT Asp 395	AAG Lys	GAA Glu	GTC Val	CAA Gln	AAG Lys 400	1200
CTC Leu	GAC Asp	AAC Asn	TTC Phe	AGC Ser 405	AAC Asn	GCC Ala	GCC Ala	CAA Gln	CTG Leu 410	GTT Val	GTC Val	GAC Asp	GGC Gly	ATT Ile 415	ATG Met	1248
ATT Ile	CCG Pro	CTC Leu	TTG Leu 420	CCC Pro	GAG Glu	GCT Ala	TCC Ser	GAA Glu 425	AGT Ser	GGG Gly	AAC Asn	AAT Asn	CAA Gln 430	GCC Ala	AAT Asn	1296

CAA Gln	GGT Gly	ACA Thr	AAT Asn	GGC Gly	GGA Gly	ACA Thr	GCC Ala	TTT Phe	ACC Thr	CGC Arg	AAA Lys	TTT Phe	GAC Asp	CAC His	ACG Thr	1344
	435						440					445				
CCG Pro	GAA Glu	AGT Ser	GAT Asp	AAA Lys	AAA Lys	GAC Asp	GCC Ala	CAA Gln	GCA Ala	GGT Gly	ACG Thr	CAG Gln	ACG Thr	AAT Asn	GGG Gly	1392
	450					455					460					
GCG Ala	CAA Gln	ACC Thr	GCT Ala	TCA Ser	AAT Asn	ACG Thr	GCA Ala	GGT Gly	GAT Asp	ACC Thr	AAT Asn	GGC Gly	AAA Lys	ACA Thr	AAA Lys	1440
	465				470					475					480	
ACC Thr	TAT Tyr	GAA Glu	GTC Val	GAA Glu	GTC Val	TGC Cys	TGT Cys	TCC Ser	AAC Asn	CTC Leu	AAT Asn	TAT Tyr	CTG Leu	AAA Lys	TAC Tyr	1488
			485						490					495		
GGA Gly	ATG Met	TTG Leu	ACG Thr	CGC Arg	AAA Lys	AAC Asn	AGC Ser	AAG Lys	TCC Ser	GCG Ala	ATG Met	CAG Gln	GCA Ala	GGA Gly	GAA Glu	1536
			500					505					510			
AGC Ser	AGT Ser	AGT Ser	CAA Gln	GCT Ala	GAT Asp	GCT Ala	AAA Lys	ACG Thr	GAA Glu	CAA Gln	GTT Val	GAA Glu	CAA Gln	AGT Ser	ATG Met	1584
		515					520					525				
TTC Phe	CTC Leu	CAA Gln	GGC Gly	GAG Glu	CGC Arg	ACC Thr	GAT Asp	GAA Glu	AAA Lys	GAG Glu	ATT Ile	CCA Pro	AGC Ser	GAG Glu	CAA Gln	1632
	530					535					540					
AAC Asn	ATC Ile	GTT Val	TAT Tyr	CGG Arg	GGG Gly	TCT Ser	TGG Trp	TAC Tyr	GGA Gly	TAT Tyr	ATT Ile	GCC Ala	AAC Asn	GAC Asp	AAA Lys	1680
545					550					555					560	
AGC Ser	ACA Thr	AGC Ser	TGG Trp	AGC Ser	GGC Gly	AAT Asn	GCT Ala	TCC Ser	AAT Asn	GCA Ala	ACG Thr	AGT Ser	GGC Gly	AAC Asn	AGG Arg	1728
			565						570					575		
GCG Ala	GAA Glu	TTT Phe	ACT Thr	GTG Val	AAT Asn	TTT Phe	GCC Ala	GAT Asp	AAA Lys	AAA Lys	ATT Ile	ACT Thr	GGT Gly	ACG Thr	TTA Leu	1776
			580					585					590			
ACC Thr	GCT Ala	GAC Asp	AAC Asn	AGG Arg	CAG Gln	GAG Glu	GCA Ala	ACC Thr	TTT Phe	ACC Thr	ATT Ile	GAT Asp	GGT Gly	AAT Asn	ATT Ile	1824
		595					600					605				
AAG Lys	GAC Asp	AAC Asn	GGC Gly	TTT Phe	GAA Glu	GGT Gly	ACG Thr	GCG Ala	AAA Lys	ACT Thr	GCT Ala	GAG Glu	TCA Ser	GGT Gly	TTT Phe	1872
	610					615					620					
GAT Asp	CTC Leu	GAT Asp	CAA Gln	AGC Ser	AAT Asn	ACC Thr	ACC Thr	CGC Arg	ACG Thr	CCT Pro	AAG Lys	GCA Ala	TAT Tyr	ATC Ile	ACA Thr	1920
	625				630					635					640	



GAT GCC AAG GTG CAG GGC GGT TTT TAC GGG CCC AAA GCC GAA GAG TTG	1968
Asp Ala Lys Val Gln Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Leu	
645 650 655	
GGC GGA TGG TTT GCC TAT CCG GGC GAT AAA CAA ACG AAA AAT GCA ACA	2016
Gly Gly Trp Phe Ala Tyr Pro Gly Asp Lys Gln Thr Lys Asn Ala Thr	
660 665 670	
AAT GCA TCC GGC AAT AGC AGT GCA ACT GTC GTA TTC GGT GCG AAA CGC	2064
Asn Ala Ser Gly Asn Ser Ser Ala Thr Val Val Phe Gly Ala Lys Arg	
675 680 685	
CAA CAG CCT GTG CGA TAACGCAAGC CCAAAAAGAC CAAGGCGGAT ACGGT	2114
Gln Gln Pro Val Arg	
690	

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 693 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Cys	Leu	Gly	Gly	Gly	Gly	Thr	Phe	Asp	Leu	Asp	Ser	Val	Asp	Thr	Glu
1				5					10					15	
Ala	Pro	Arg	Pro	Asp	Pro	Lys	Tyr	Gln	Asp	Val	Ser	Ser	Glu	Lys	Pro
			20					25					30		
Gln	Ala	Gln	Lys	Asp	Gln	Gly	Gly	Tyr	Gly	Phe	Ala	Met	Arg	Leu	Lys
		35					40					45			
Arg	Arg	Asn	Trp	Tyr	Ser	Ala	Ala	Lys	Glu	Asp	Glu	Val	Lys	Leu	Asn
	50					55					60				
Glu	Ser	Asp	Trp	Glu	Thr	Thr	Gly	Leu	Pro	Thr	Glu	Pro	Lys	Lys	Leu
65				70						75					80
Pro	Leu	Lys	Gln	Glu	Ser	Val	Ile	Ser	Lys	Val	Gln	Ala	Asn	Asn	Gly
				85					90					95	
Asp	Asn	Asn	Ile	Tyr	Thr	Ser	Pro	Tyr	Leu	Thr	Gln	Ser	Asn	His	Gln
			100					105					110		
Asn	Ser	Ser	Ile	Asn	Gly	Gly	Ala	Asn	Leu	Pro	Lys	Asn	Glu	Val	Thr
		115					120					125			
Asn	Tyr	Lys	Asp	Phe	Lys	Tyr	Val	Tyr	Ser	Gly	Trp	Phe	Tyr	Lys	His
	130					135					140				

Ala	Lys	Asn	Glu	Ile	Ile	Arg	Glu	Asn	Ser	Ser	Ile	Lys	Gly	Ala	Lys	145	150	155	160
Asn	Gly	Asp	Asp	Gly	Tyr	Ile	Phe	Tyr	His	Gly	Lys	Glu	Pro	Ser	Arg	165	170	175	
Gln	Leu	Pro	Ala	Ser	Gly	Thr	Val	Thr	Tyr	Lys	Gly	Val	Trp	His	Phe	180	185	190	
Ala	Thr	Asp	Val	Lys	Lys	Ser	Gln	Asn	Phe	Arg	Asp	Ile	Ile	Gln	Pro	195	200	205	
Ser	Lys	Lys	Gln	Gly	Asp	Arg	Tyr	Ser	Gly	Phe	Ser	Gly	Asp	Asp	Asp	210	215	220	
Glu	Gln	Tyr	Ser	Asn	Lys	Asn	Glu	Ser	Met	Leu	Lys	Asp	Gly	Gln	Glu	225	230	235	240
Gly	Tyr	Gly	Phe	Thr	Ser	Asn	Leu	Glu	Val	Asp	Phe	Gly	Ser	Lys	Lys	245	250	255	
Leu	Thr	Gly	Lys	Leu	Ile	Arg	Asn	Asn	Arg	Val	Thr	Asn	Ala	Pro	Thr	260	265	270	
Asn	Asp	Lys	Tyr	Thr	Thr	Gln	Tyr	Tyr	Ser	Leu	Asp	Ala	Gln	Ile	Thr	275	280	285	
Gly	Asn	Arg	Phe	Asn	Gly	Lys	Ala	Ile	Arg	Thr	Asp	Lys	Pro	Asp	Thr	290	295	300	
Gly	Gly	Thr	Lys	Leu	His	Pro	Phe	Val	Ser	Asp	Ser	Ser	Ser	Leu	Ser	305	310	315	320
Gly	Gly	Phe	Phe	Gly	Pro	Lys	Gly	Glu	Glu	Leu	Gly	Phe	Arg	Phe	Leu	325	330	335	
Ser	Asp	Asp	Lys	Lys	Val	Ala	Val	Val	Gly	Ser	Ala	Lys	Thr	Lys	Asp	340	345	350	
Lys	Thr	Glu	Asn	Gly	Ala	Val	Ala	Ser	Gly	Gly	Thr	Asp	Ala	Ala	Ala	355	360	365	
Ser	Asn	Gly	Ala	Ala	Gly	Thr	Ser	Ser	Glu	Asn	Ser	Lys	Leu	Thr	Thr	370	375	380	
Val	Leu	Asp	Ala	Val	Glu	Leu	Lys	Leu	Gly	Asp	Lys	Glu	Val	Gln	Lys	385	390	395	400
Leu	Asp	Asn	Phe	Ser	Asn	Ala	Ala	Gln	Leu	Val	Val	Asp	Gly	Ile	Met	405	410	415	
Ile	Pro	Leu	Leu	Pro	Glu	Ala	Ser	Glu	Ser	Gly	Asn	Asn	Gln	Ala	Asn	420	425	430	

Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe Asp His Thr  
 435 440 445  
 Pro Glu Ser Asp Lys Lys Asp Ala Gln Ala Gly Thr Gln Thr Asn Gly  
 450 455 460  
 Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly Lys Thr Lys  
 465 470 475 480  
 Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr Leu Lys Tyr  
 485 490 495  
 Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln Ala Gly Glu  
 500 505 510  
 Ser Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln Val Glu Gln Ser Met  
 515 520 525  
 Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro Ser Glu Gln  
 530 535 540  
 Asn Ile Val Tyr Arg Gly Ser Trp Tyr Gly Tyr Ile Ala Asn Asp Lys  
 545 550 555 560  
 Ser Thr Ser Trp Ser Gly Asn Ala Ser Asn Ala Thr Ser Gly Asn Arg  
 565 570 575  
 Ala Glu Phe Thr Val Asn Phe Ala Asp Lys Lys Ile Thr Gly Thr Leu  
 580 585 590  
 Thr Ala Asp Asn Arg Gln Glu Ala Thr Phe Thr Ile Asp Gly Asn Ile  
 595 600 605  
 Lys Asp Asn Gly Phe Glu Gly Thr Ala Lys Thr Ala Glu Ser Gly Phe  
 610 615 620  
 Asp Leu Asp Gln Ser Asn Thr Thr Arg Thr Pro Lys Ala Tyr Ile Thr  
 625 630 635 640  
 Asp Ala Lys Val Gln Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Leu  
 645 650 655  
 Gly Gly Trp Phe Ala Tyr Pro Gly Asp Lys Gln Thr Lys Asn Ala Thr  
 660 665 670  
 Asn Ala Ser Gly Asn Ser Ser Ala Thr Val Val Phe Gly Ala Lys Arg  
 675 680 685  
 Gln Gln Pro Val Arg  
 690

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2114 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: N. meningitidis
- (B) STRAIN: S3032

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..2097

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..2097

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TGT	TTG	GGC	GGA	GGC	GGC	GGC	AGT	TTC	GAT	CTT	GAT	TCT	GTC	GAT	ACC	48
Cys	Leu	Gly	Gly	Gly	Gly	Gly	Ser	Phe	Asp	Leu	Asp	Ser	Val	Asp	Thr	
1				5					10					15		
GAA	GCC	CCG	CGT	CCC	GCG	CCA	AAG	TAT	CAA	GAT	GTT	TCT	TCC	GAA	AAA	96
Glu	Ala	Pro	Arg	Pro	Ala	Pro	Lys	Tyr	Gln	Asp	Val	Ser	Ser	Glu	Lys	
			20					25					30			
CCG	CAA	GCC	CAA	AAA	GAC	CAA	GGC	GGA	TAC	GGT	TTT	GCG	ATG	AGG	TTG	144
Pro	Gln	Ala	Gln	Lys	Asp	Gln	Gly	Gly	Tyr	Gly	Phe	Ala	Met	Arg	Leu	
		35					40					45				
AAA	CGG	AGG	AAT	TGG	TAT	CCG	TCG	GCA	AAA	GAA	AAC	GAG	GTT	AAA	CTG	192
Lys	Arg	Arg	Asn	Trp	Tyr	Pro	Ser	Ala	Lys	Glu	Asn	Glu	Val	Lys	Leu	
	50					55					60					
AAT	GAG	AGT	GAT	TGG	GAG	ACG	ACA	GGA	TTG	CCA	AGC	AAT	CCC	AAA	AAC	240
Asn	Glu	Ser	Asp	Trp	Gln	Thr	Thr	Gly	Leu	Pro	Ser	Asn	Pro	Lys	Asn	
	65			70					75					80		
TTA	CCT	GAG	CGA	CAG	AAA	TCG	GTT	ATT	GAT	CAA	GTA	GAA	ACA	GAT	GGC	288
Leu	Pro	Glu	Arg	Gln	Lys	Ser	Val	Ile	Asp	Gln	Val	Glu	Thr	Asp	Gly	
			85					90					95			
GAC	AGC	AAT	AAC	AGC	AAT	ATT	TAT	TCT	TCC	CCC	TAT	CTC	ACG	CAA	TCA	336
Asp	Ser	Asn	Asn	Ser	Asn	Ile	Tyr	Ser	Ser	Pro	Tyr	Leu	Thr	Gln	Ser	
		100						105					110			

AAC Asn	CAT His	CAA Gln 115	AAC Asn	GGC Gly	AAC Asn	ACT Thr	GGC Gly 120	AAC Asn	GGT Gly	GTA Val	AAC Asn	CAA Gln 125	CCA Pro	AAA Lys	AAC Asn	384
GAA Glu 130	GTA Val	ACA Thr	GAT Asp	TAC Tyr	AAA Lys	AAT Asn 135	TTT Phe	AAA Lys	TAT Tyr	GTT Val	TAT Tyr 140	TCC Ser	GGC Gly	TGG Trp	TTT Phe	432
TAC Tyr 145	AAA Lys	CAC His	GCC Ala	AAA Lys	CGA Arg 150	GAG Glu	GTT Val	AAC Asn	TTA Leu	GCG Ala 155	GTG Val	GAA Glu	CCT Pro	AAA Lys	ATT Ile 160	480
GCA Ala	AAA Lys	AAC Asn	GGC Gly	GAC Asp 165	GAC Asp	GGT Gly	TAT Tyr	ATC Ile	TTC Phe 170	TAT Tyr	CAC His	GGT Gly	AAA Lys	GAC Asp 175	CCT Pro	528
TCC Ser	CGA Arg	CAA Gln	CTT Leu 180	CCC Pro	GCT Ala	TCT Ser	GGA Gly 185	AAA Lys	ATT Ile	ACC Thr	TAT Tyr	AAA Lys 190	GGT Gly	GTG Val	TGG Trp	576
CAT His	TTT Phe 195	GCG Ala	ACC Thr	GAT Asp	ACA Thr	AAA Lys 200	AGG Arg	GGT Gly	CAA Gln	AAA Lys	TTT Phe 205	CGT Arg	GAA Glu	ATT Ile	ATC Ile	624
CAA Gln 210	CCT Pro	TCA Ser	AAA Lys	AAT Asn	CAA Gln	GGC Gly 215	GAC Asp	AGA Arg	TAT Tyr	AGC Ser	GGA Gly 220	TTT Phe	TCG Ser	GGT Gly	GAT Asp	672
GAT Asp 225	GAT Asp	GAA Glu	CAA Gln	TAT Tyr	TCT Ser 230	AAT Asn	AAA Lys	AAC Asn	GAA Glu 235	TCC Ser	ATG Met	CTG Leu	AAA Lys	GAT Asp	GGT Gly 240	720
CAT His	GAA Glu	GGT Gly	TAT Tyr 245	GGT Gly	TTT Phe	GCC Ala	TCG Ser	AAT Asn 250	TTA Leu	GAA Glu	GTG Val	GAT Asp	TTC Phe	GAC Asp 255	AAT Asn	768
AAA Lys	AAA Lys	TTG Leu 260	ACG Thr	GGT Gly	AAA Lys	TTA Leu	ATA Ile 265	CGC Arg	AAT Asn	AAT Asn	GCG Ala	AAC Asn	CAA Gln 270	AAT Asn	AAT Asn	816
AAT Asn	ACT Thr 275	AAT Asn	AAT Asn	GAC Asp	AAA Lys	CAC His	ACC Thr 280	ACC Thr	CAA Gln	TAC Tyr	TAC Tyr	AGC Ser 285	CTT Leu	GAT Asp	GCG Ala	864
ACG Thr 290	CTT Leu	AAG Lys	GGA Gly	AAC Asn	CGC Arg	TTC Phe 295	AGC Ser	GGA Gly	AAA Lys	GCG Ala	GAA Glu 300	GCA Ala	ACC Thr	GAC Asp	AAA Lys	912
CCC Pro 305	AAA Lys	AAC Asn	GAC Asp	GGC Gly	GAA Glu 310	ACC Thr	AAG Lys	GAA Glu	CAT His	CCC Pro 315	TTT Phe	GTT Val	TCC Ser	GAC Asp	TCG Ser 320	960

6 cont

TCT	TCT	TTG	AGC	GGC	GGC	TTT	TTC	GGC	CCG	CAG	GGT	GAG	GAA	TTG	GGT	1008
Ser	Ser	Leu	Ser	Gly	Gly	Phe	Phe	Gly	Pro	Gln	Gly	Glu	Glu	Leu	Gly	
				325					330					335		
TTC	CGC	TTT	TTG	AGC	AAC	GAT	CAA	AAA	GTT	GCC	GTT	GTC	GGC	AGC	GCG	1056
Phe	Arg	Phe	Leu	Ser	Asn	Asp	Gln	Lys	Val	Ala	Val	Val	Gly	Ser	Ala	
			340					345					350			
AAA	ACC	AAA	GAC	AAA	CCC	GCA	AAT	GGC	AAT	ACT	GCG	GAG	GCT	TCA	GGC	1104
Lys	Thr	Lys	Asp	Lys	Pro	Ala	Asn	Gly	Asn	Thr	Ala	Glu	Ala	Ser	Gly	
		355					360					365				
GGC	ACA	GAT	GCG	GCA	GCA	TCG	GGC	GGT	GCG	GCA	GGC	ACG	TCG	TCT	GAA	1152
Gly	Thr	Asp	Ala	Ala	Ala	Ser	Gly	Gly	Ala	Ala	Gly	Thr	Ser	Ser	Glu	
	370					375					380					
AAC	AGT	AAG	CTG	ACC	ACG	GTT	TTG	GAT	GCG	GTC	GAG	CTG	ACG	CAC	GGC	1200
Asn	Ser	Lys	Leu	Thr	Thr	Val	Leu	Asp	Ala	Val	Glu	Leu	Thr	His	Gly	
385					390					395					400	
GGC	ACA	GCA	ATC	AAA	AAT	CTC	GAC	AAC	TTC	AGC	AAT	GCC	GCC	CAA	CTG	1248
Gly	Thr	Ala	Ile	Lys	Asn	Leu	Asp	Asn	Phe	Ser	Asn	Ala	Ala	Gln	Leu	
			405						410					415		
GTT	GTC	GAC	GGC	ATT	ATG	ATT	CCG	CTC	CTG	CCT	CAA	AAT	TCA	ACA	GGC	1296
Val	Val	Asp	Gly	Ile	Met	Ile	Pro	Leu	Leu	Pro	Gln	Asn	Ser	Thr	Gly	
			420					425					430			
AAA	AAT	AAT	CAG	CCC	GAT	CAA	GGT	AAA	AAC	GGC	GGA	ACA	GCC	TTT	ATC	1344
Lys	Asn	Asn	Gln	Pro	Asp	Gln	Gly	Lys	Asn	Gly	Gly	Thr	Ala	Phe	Ile	
		435					440					445				
TAT	AAA	ACG	ACC	TAC	ACG	CCG	AAA	AAC	GAT	GAC	AAA	GAT	ACC	AAA	GCC	1392
Tyr	Lys	Thr	Thr	Tyr	Thr	Pro	Lys	Asn	Asp	Asp	Lys	Asp	Thr	Lys	Ala	
	450					455					460					
CAA	ACA	GTC	ACG	GGC	GGC	ACG	CAA	ACC	GCT	TCA	AAT	ACG	GCA	GGT	GAT	1440
Gln	Thr	Val	Thr	Gly	Gly	Thr	Gln	Thr	Ala	Ser	Asn	Thr	Ala	Gly	Asp	
465				470					475						480	
GCC	AAT	GGC	AAA	ACA	AAA	AAC	TAT	GAA	GTC	GAA	GTC	TGC	TGT	TCC	AAC	1488
Ala	Asn	Gly	Lys	Thr	Lys	Thr	Tyr	Glu	Val	Glu	Val	Cys	Cys	Ser	Asn	
			485					490						495		
CTC	AAT	TAT	CTG	AAA	TAC	GGG	TTG	CTG	ACG	CGC	AAA	ACT	GCC	GGC	AAC	1536
Leu	Asn	Tyr	Leu	Lys	Tyr	Gly	Leu	Leu	Thr	Arg	Lys	Thr	Ala	Gly	Asn	
			500				505						510			
ACG	GTG	GGA	AGC	GGC	AAC	AGC	AGC	CCA	ACC	GCC	GCC	GCC	CAA	ACG	GAC	1584
Thr	Val	Gly	Ser	Gly	Asn	Ser	Ser	Pro	Thr	Ala	Ala	Ala	Gln	Thr	Asp	
		515					520					525				

Glu	Val	Lys	Asp	Tyr	Lys	Asn	Phe	Lys	Tyr	Val	Tyr	Ser	Gly	Trp	Phe	
125					130					135					140	
Tyr	Lys	His	Ala	Glu	Ser	Glu	Arg	Glu	Phe	Ser	Lys	Ile	Lys	Phe	Lys	
				145					150					155		
Ser	Gly	Asp	Asp	Gly	Tyr	Ile	Phe	Tyr	His	Gly	Lys	Asp	Pro	Ser	Arg	
			160					165					170			
Gln	Leu	Pro	Thr	Ser	Glu	Lys	Val	Ile	Tyr	Lys	Gly	Val	Trp	His	Phe	
		175					180					185				
Val	Thr	Asp	Thr	Glu	Lys	Gly	Gln	Lys	Phe	Asn	Asp	Ile	Leu	Glu	Thr	
	190					195					200					
Ser	Lys	Gly	Gln	Gly	Asp	Arg	Tyr	Ser	Gly	Phe	Ser	Gly	Asp	Asp	Gly	
205					210					215					220	
Glu	Thr	Thr	Ser	Asn	Arg	Thr	Asp	Ser	Asn	Leu	Asn	Asp	Lys	His	Glu	
				225					230					235		
Gly	Tyr	Gly	Phe	Thr	Ser	Asn	Leu	Glu	Val	Asp	Phe	Gly	Ser	Lys	Lys	
			240					245					250			
Leu	Thr	Gly	Lys	Leu	Ile	Arg	Asn	Asn	Arg	Val	Thr	Asn	Ala	Thr	Thr	
		255					260					265				
Asn	Asp	Lys	Tyr	Thr	Thr	Gln	Tyr	Tyr	Ser	Leu	Asp	Ala	Gln	Ile	Thr	
	270					275					280					
Gly	Asn	Arg	Phe	Asn	Gly	Lys	Ala	Ile	Ala	Thr	Asp	Lys	Pro	Asp	Thr	
285					290					295					300	
Gly	Gly	Thr	Lys	Leu	His	Pro	Phe	Val	Ser	Asp	Ser	Ser	Ser	Leu	Ser	
				305					310					315		
Gly	Gly	Phe	Phe	Gly	Pro	Lys	Gly	Glu	Glu	Leu	Gly	Phe	Arg	Phe	Leu	
			320					325					330			
Ser	Asp	Asp	Lys	Lys	Val	Ala	Val	Val	Gly	Ser	Ala	Lys	Thr	Lys	Asp	
		335					340					345				
Lys	Thr	Glu	Asn	Gly	Ala	Val	Ala	Ser	Gly	Gly	Thr	Asp	Ala	Ala	Ala	
	350					355					360					
Ser	Asn	Gly	Ala	Ala	Gly	Thr	Ser	Ser	Glu	Asn	Ser	Lys	Leu	Thr	Thr	
365					370					375					380	
Val	Leu	Asp	Ala	Val	Glu	Leu	Lys	Leu	Gly	Asp	Lys	Glu	Val	Gln	Lys	
				385					390					395		
Leu	Asp	Asn	Phe	Ser	Asn	Ala	Ala	Gln	Leu	Val	Val	Asp	Gly	Ile	Met	
			400					405					410			

[illegible]



(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Thr Lys Asp Lys Leu Glu Asn Gly Ala Ala Ala Ser Gly Ser Thr Gly  
1 5 10 15  
Ala Ala Ala Ser Gly Gly Ala Ala Asp Met Pro Ser Glu Asn Gly Lys  
20 25 30  
Leu Thr Thr Val Leu Asp Ala Val Glu Leu Lys Ser Gly Gly Lys Glu  
35 40 45  
Val Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp  
50 55 60  
Gly Ile Met Ile Pro Leu Leu Pro Lys Asn Ser Glu Ser Glu Ser Asn  
65 70 75 80  
Gln Ala Asp Lys Gly Lys Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe  
85 90 95  
Glu His Thr Pro Glu Ser Asp Lys Lys Asp Thr Gln Ala Gly Thr Ala  
100 105 110  
Glu Asn Gly Asn Pro Ala Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly  
115 120 125  
Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr  
130 135 140  
Leu Lys Tyr Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln  
145 150 155 160  
Ala Gly Glu Asn Gly Ser Leu Ala Asp Ala Lys Thr Glu Gln Val Glu  
165 170 175  
Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro  
180 185 190  
Lys Glu Gln Gln Asp Ile Val  
195

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Thr Lys Asp Lys Thr Glu Asn Gly Ala Val Ala Ser Gly Gly Thr Asp  
1 5 10 15  
Ala Ala Ala Ser Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn Ser Lys  
20 25 30  
Leu Thr Thr Val Leu Asp Ala Val Glu Leu Lys Leu Gly Asp Lys Glu  
35 40 45  
Val Gln Lys Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp  
50 55 60  
Gly Ile Met Ile Pro Leu Leu Pro Glu Thr Ser Glu Ser Gly Asn Asn  
65 70 75 80  
Gln Ala Asn Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe  
85 90 95  
Asp His Thr Pro Glu Ser Asp Lys Lys Asp Ala Gln Ala Gly Thr Gln  
100 105 110  
Thr Asn Gly Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly  
115 120 125  
Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr  
130 135 140  
Leu Lys Tyr Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln  
145 150 155 160  
Ala Gly Glu Ser Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln Val Gly  
165 170 175  
Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro  
180 185 190  
Ser Glu Gln Asn Ile Val  
195

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Thr Lys Asp Asn Thr Ala Asn Gly Asn Thr Ala Ala Ala Ser Gly Gly  
1 5 10 15  
Thr Asp Ala Ala Ala Ser Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn  
20 25 30  
Gly Lys Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr Leu Asn Asp  
35 40 45  
Lys Lys Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val  
50 55 60  
Val Asp Gly Ile Met Ile Pro Leu Leu Pro Glu Ala Ser Glu Ser Gly  
65 70 75 80  
Asn Asn Gln Ala Asn Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg  
85 90 95  
Lys Phe Ala His Thr Pro Lys Ser Asp Glu Lys Asp Thr His Ala Gly  
100 105 110  
Thr Ala Ala Asn Gly Asp Gln Ala Ala Ser Asn Thr Ala Gly Asp Thr  
115 120 125  
Asn Gly Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu  
130 135 140  
Asn Tyr Leu Lys Tyr Gly Leu Leu Thr Arg Lys Thr Ala Gly Asn Thr  
145 150 155 160  
Gly Glu Gly Gly Asn Gly Ser Gln Thr Ala Ala Ala Gln Thr Ala Gln  
165 170 175  
Gly Ala Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu  
180 185 190  
Ile Pro Ser Glu Gln Asn Val  
195

GCG	CAG	AGT	ATG	TTC	CTC	CAA	GGC	GAG	CGC	ACC	GAT	GAA	AAC	AAG	ATT	1632
Ala	Gln	Ser	Met	Phe	Leu	Gln	Gly	Glu	Arg	Thr	Asp	Glu	Asn	Lys	Ile	
530						535					540					
CCA	AGC	GAG	CAA	AAC	GTC	GTT	TAT	CGG	GGG	TCT	TGG	TAC	GGG	CAT	ATT	1680
Pro	Ser	Glu	Gln	Asn	Val	Val	Tyr	Arg	Gly	Ser	Trp	Tyr	Gly	His	Ile	
545					550					555					560	
GCC	AGC	AGC	ACA	AGC	TGG	AGC	GGC	AAT	GCT	TCT	GAT	AAA	GAG	GGC	GGC	1728
Ala	Ser	Ser	Thr	Ser	Trp	Ser	Gly	Asn	Ala	Ser	Asp	Lys	Glu	Gly	Gly	
				565					570					575		
AAC	AGG	GCG	GAA	TTT	ACT	GTG	AAT	TTT	GGC	GAG	AAA	AAA	ATT	ACC	GGC	1776
Asn	Arg	Ala	Glu	Phe	Thr	Val	Asn	Phe	Gly	Glu	Lys	Lys	Ile	Thr	Gly	
			580					585					590			
ACG	TTA	ACC	GCT	GAA	AAC	AGG	CAG	GAG	GCA	ACC	TTT	ACC	ATT	GAT	GGT	1824
Thr	Leu	Thr	Ala	Glu	Asn	Arg	Gln	Glu	Ala	Thr	Phe	Thr	Ile	Asp	Gly	
		595					600					605				
AAG	ATT	GAG	GGC	AAC	GGT	TTT	TCC	GGT	ACG	GCA	AAA	ACT	GCT	GAA	TTA	1872
Lys	Ile	Glu	Gly	Asn	Gly	Phe	Ser	Gly	Thr	Ala	Lys	Thr	Ala	Glu	Leu	
610						615					620					
GGT	TTT	GAT	CTC	GAT	CAA	AAA	AAT	ACC	ACC	CGC	ACG	CCT	AAG	GCA	TAT	1920
Gly	Phe	Asp	Leu	Asp	Gln	Lys	Asn	Thr	Thr	Arg	Thr	Pro	Lys	Ala	Tyr	
625					630					635					640	
ATC	ACA	GAT	GCC	AAG	GTA	AAG	GGC	GGT	TTT	TAC	GGG	CCC	AAA	GCC	GAA	1968
Ile	Thr	Asp	Ala	Lys	Val	Lys	Gly	Gly	Phe	Tyr	Gly	Pro	Lys	Ala	Glu	
				645					650					655		
GAG	TTG	GGC	GGA	TGG	TTT	GCC	TAT	TCG	GAC	GAT	AAA	CAA	ACG	AAA	AAT	2016
Glu	Leu	Gly	Gly	Trp	Phe	Ala	Tyr	Ser	Asp	Asp	Lys	Gln	Thr	Lys	Asn	
			660					665					670			
GCA	ACA	GAT	GCA	TCC	GGC	AAT	GGA	AAT	TCA	GCA	AGC	AGT	GCA	ACT	GTC	2064
Ala	Thr	Asp	Ala	Ser	Gly	Asn	Gly	Asn	Ser	Ala	Ser	Ser	Ala	Thr	Val	
		675					680					685				
GTA	TTC	GGT	GCG	AAA	CGC	CAA	CAG	CCT	GTG	CAA	TAAACCAAGG	CGGATAC				2114
Val	Phe	Gly	Ala	Lys	Arg	Gln	Gln	Pro	Val	Gln						
690						695										

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 699 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Cys Leu Gly Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser Val Asp Thr  
1 5 10 15  
Glu Ala Pro Arg Pro Ala Pro Lys Tyr Gln Asp Val Ser Ser Glu Lys  
20 25 30  
Pro Gln Ala Gln Lys Asp Gln Gly Gly Tyr Gly Phe Ala Met Arg Leu  
35 40 45  
Lys Arg Arg Asn Trp Tyr Pro Ser Ala Lys Glu Asn Glu Val Lys Leu  
50 55 60  
Asn Glu Ser Asp Trp Glu Thr Thr Gly Leu Pro Ser Asn Pro Lys Asn  
65 70 75 80  
Leu Pro Glu Arg Gln Lys Ser Val Ile Asp Gln Val Glu Thr Asp Gly  
85 90 95  
Asp Ser Asn Asn Ser Asn Ile Tyr Ser Ser Pro Tyr Leu Thr Gln Ser  
100 105 110  
Asn His Gln Asn Gly Asn Thr Gly Asn Gly Val Asn Gln Pro Lys Asn  
115 120 125  
Glu Val Thr Asp Tyr Lys Asn Phe Lys Tyr Val Tyr Ser Gly Trp Phe  
130 135 140  
Tyr Lys His Ala Lys Arg Glu Val Asn Leu Ala Val Glu Pro Lys Ile  
145 150 155 160  
Ala Lys Asn Gly Asp Asp Gly Tyr Ile Phe Tyr His Gly Lys Asp Pro  
165 170 175  
Ser Arg Gln Leu Pro Ala Ser Gly Lys Ile Thr Tyr Lys Gly Val Trp  
180 185 190  
His Phe Ala Thr Asp Thr Lys Arg Gly Gln Lys Phe Arg Glu Ile Ile  
195 200 205  
Gln Pro Ser Lys Asn Gln Gly Asp Arg Tyr Ser Gly Phe Ser Gly Asp  
210 215 220  
Asp Asp Glu Gln Tyr Ser Asn Lys Asn Glu Ser Met Leu Lys Asp Gly  
225 230 235 240  
His Glu Gly Tyr Gly Phe Ala Ser Asn Leu Glu Val Asp Phe Asp Asn  
245 250 255  
Lys Lys Leu Thr Gly Lys Leu Ile Arg Asn Asn Ala Asn Gln Asn Asn  
260 265 270

Asn	Thr	Asn	Asn	Asp	Lys	His	Thr	Thr	Gln	Tyr	Tyr	Ser	Leu	Asp	Ala	
		275					280					285				
Thr	Leu	Lys	Gly	Asn	Arg	Phe	Ser	Gly	Lys	Ala	Glu	Ala	Thr	Asp	Lys	
	290					295					300					
Pro	Lys	Asn	Asp	Gly	Glu	Thr	Lys	Glu	His	Pro	Phe	Val	Ser	Asp	Ser	
305					310					315					320	
Ser	Ser	Leu	Ser	Gly	Gly	Phe	Phe	Gly	Pro	Gln	Gly	Glu	Glu	Leu	Gly	
				325					330					335		
Phe	Arg	Phe	Leu	Ser	Asn	Asp	Gln	Lys	Val	Ala	Val	Val	Gly	Ser	Ala	
			340					345					350			
Lys	Thr	Lys	Asp	Lys	Pro	Ala	Asn	Gly	Asn	Thr	Ala	Glu	Ala	Ser	Gly	
		355					360					365				
Gly	Thr	Asp	Ala	Ala	Ala	Ser	Gly	Gly	Ala	Ala	Gly	Thr	Ser	Ser	Glu	
	370					375					380					
Asn	Ser	Lys	Leu	Thr	Thr	Val	Leu	Asp	Ala	Val	Glu	Leu	Thr	His	Gly	
385					390					395					400	
Gly	Thr	Ala	Ile	Lys	Asn	Leu	Asp	Asn	Phe	Ser	Asn	Ala	Ala	Gln	Leu	
			405						410					415		
Val	Val	Asp	Gly	Ile	Met	Ile	Pro	Leu	Leu	Pro	Gln	Asn	Ser	Thr	Gly	
			420					425					430			
Lys	Asn	Asn	Gln	Pro	Asp	Gln	Gly	Lys	Asn	Gly	Gly	Thr	Ala	Phe	Ile	
		435					440					445				
Tyr	Lys	Thr	Thr	Tyr	Thr	Pro	Lys	Asn	Asp	Asp	Lys	Asp	Thr	Lys	Ala	
	450					455					460					
Gln	Thr	Val	Thr	Gly	Gly	Thr	Gln	Thr	Ala	Ser	Asn	Thr	Ala	Gly	Asp	
465					470					475					480	
Ala	Asn	Gly	Lys	Thr	Lys	Thr	Tyr	Glu	Val	Glu	Val	Cys	Cys	Ser	Asn	
				485					490					495		
Leu	Asn	Tyr	Leu	Lys	Tyr	Gly	Leu	Leu	Thr	Arg	Lys	Thr	Ala	Gly	Asn	
		500					505						510			
Thr	Val	Gly	Ser	Gly	Asn	Ser	Ser	Pro	Thr	Ala	Ala	Ala	Gln	Thr	Asp	
		515					520					525				
Ala	Gln	Ser	Met	Phe	Leu	Gln	Gly	Glu	Arg	Thr	Asp	Glu	Asn	Lys	Ile	
	530					535					540					
Pro	Ser	Glu	Gln	Asn	Val	Val	Tyr	Arg	Gly	Ser	Trp	Tyr	Gly	His	Ile	
545					550					555					560	

Ala Ser Ser Thr Ser Trp Ser Gly Asn Ala Ser Asp Lys Glu Gly Gly  
565 570 575

Asn Arg Ala Glu Phe Thr Val Asn Phe Gly Glu Lys Lys Ile Thr Gly  
580 585 590

Thr Leu Thr Ala Glu Asn Arg Gln Glu Ala Thr Phe Thr Ile Asp Gly  
595 600 605

Lys Ile Glu Gly Asn Gly Phe Ser Gly Thr Ala Lys Thr Ala Glu Leu  
610 615 620

Gly Phe Asp Leu Asp Gln Lys Asn Thr Thr Arg Thr Pro Lys Ala Tyr  
625 630 635 640

Ile Thr Asp Ala Lys Val Lys Gly Gly Phe Tyr Gly Pro Lys Ala Glu  
645 650 655

Glu Leu Gly Gly Trp Phe Ala Tyr Ser Asp Asp Lys Gln Thr Lys Asn  
660 665 670

Ala Thr Asp Ala Ser Gly Asn Gly Asn Ser Ala Ser Ser Ala Thr Val  
675 680 685

Val Phe Gly Ala Lys Arg Gln Gln Pro Val Gln  
690 695

(2) INFORMATION FOR SEQ ID NO:11:

*B1*  
*cont.* (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *N. meningitidis*
- (B) STRAIN: IM2169

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Thr Lys Asp Lys Leu Glu Asn Gly Ala Ala Ala Ser Gly Ser Thr Gly  
1 5 10 15

Ala Ala Ala Ser Gly Gly Ala Ala Gly Thr Ser Ser Glu Asn Ser Lys  
20 25 30

Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr Leu Asn Asp Lys Lys  
35 40 45

Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp  
 50 55 60  
 Gly Ile Met Ile Pro Leu Leu Pro Lys Asp Ser Glu Ser Gly Asn Thr  
 65 70 75 80  
 Gln Ala Asp Lys Gly Lys Asn Gly Gly Thr Glu Phe Thr Arg Lys Phe  
 85 90 95  
 Glu His Thr Pro Glu Ser Asp Lys Lys Asp Ala Gln Ala Gly Thr Gln  
 100 105 110  
 Thr Asn Gly Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly  
 115 120 125  
 Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr  
 130 135 140  
 Leu Lys Tyr Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln  
 145 150 155 160  
 Ala Gly Gly Asn Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln Val Glu  
 165 170 175  
 Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro  
 180 185 190  
 Thr Asp Gln Asn Val Val  
 195

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: N. meningitidis
- (B) STRAIN: 6940

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Thr Lys Asp Lys Thr Glu Asn Gly Ala Val Ala Ser Gly Gly Thr Asp  
 1 5 10 15  
 Ala Ala Ala Ser Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn Ser Lys  
 20 25 30  
 Leu Thr Thr Val Leu Asp Ala Val Glu Leu Lys Leu Gly Asp Lys Glu  
 35 40 45



Val Gln Lys Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp  
 50 55 60  
 Gly Ile Met Ile Pro Leu Leu Pro Glu Ala Ser Glu Ser Gly Asn Asn  
 65 70 75 80  
 Gln Ala Asn Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe  
 85 90 95  
 Asp His Thr Pro Glu Ser Asp Lys Lys Asp Ala Gln Ala Gly Thr Gln  
 100 105 110  
 Thr Asn Gly Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly  
 115 120 125  
 Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr  
 130 135 140  
 Leu Lys Tyr Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln  
 145 150 155 160  
 Ala Gly Glu Ser Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln Val Glu  
 165 170 175  
 Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro  
 180 185 190  
 Ser Glu Gln Asn Ile Val  
 195

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *N. meningitidis*
- (B) STRAIN: 2223

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Thr Lys Asp Lys Thr Glu Asn Gly Ala Val Ala Ser Gly Gly Thr Asp  
 1 5 10 15  
 Ala Ala Ala Ser Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn Ser Lys  
 20 25 30  
 Leu Thr Thr Val Leu Asp Ala Val Glu Leu Lys Leu Gly Asp Lys Glu  
 35 40 45

Val Gln Lys Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp  
 50 55 60  
 Gly Ile Met Ile Pro Leu Leu Pro Glu Ala Ser Glu Ser Gly Asn Asn  
 65 70 75 80  
 Gln Ala Asn Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe  
 85 90 95  
 Asp His Thr Pro Glu Ser Asp Lys Lys Asp Ala Gln Ala Gly Thr Gln  
 100 105 110  
 Ala Asn Gly Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly  
 115 120 125  
 Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr  
 130 135 140  
 Leu Lys Tyr Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln  
 145 150 155 160  
 Ala Gly Glu Ser Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln Val Gly  
 165 170 175  
 Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro  
 180 185 190  
 Ser Glu Gln Asn Ile Val  
 195

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: N. meningitidis
- (B) STRAIN: C708

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Thr Gln Asp Lys Pro Arg Asn Gly Ala Val Ala Ser Gly Gly Thr Gly  
 1 5 10 15  
 Ala Ala Arg Ser Asn Gly Ala Ala Gly Gln Ser Ser Glu Asn Ser Lys  
 20 25 30  
 Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr Leu Asn Asp Lys Lys  
 35 40 45

Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp  
 50 55 60  
 Gly Ile Met Ile Pro Leu Leu Pro Glu Ala Ser Glu Ser Gly Lys Asn  
 65 70 75 80  
 Gln Ala Asn Gln Gly Thr Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe  
 85 90 95  
 Asn His Thr Pro Lys Ser Asp Glu Lys Asp Thr Gln Ala Gly Thr Ala  
 100 105 110  
 Glu Asn Gly Asn Pro Ala Ala Ser Asn Thr Ala Gly Asp Ala Asn Gly  
 115 120 125  
 Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr  
 130 135 140  
 Leu Lys Tyr Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln  
 145 150 155 160  
 Ala Gly Glu Ser Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln Val Gly  
 165 170 175  
 Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro  
 180 185 190  
 Asn Asp Gln Asn Val Val  
 195

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: N. meningitidis
- (B) STRAIN: M978

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Thr Gln Asp Lys Ala Ala Asn Gly Asn Thr Ala Ala Ala Ser Gly Gly  
 1 5 10 15  
 Thr Asp Ala Ala Ala Ser Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn  
 20 25 30  
 Ser Lys Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr Leu Asn Asp  
 35 40 45

Lys Lys Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val  
 50 55 60  
 Val Asp Gly Ile Met Ile Pro Leu Leu Pro Glu Thr Ser Glu Ser Gly  
 65 70 75 80  
 Ser Asn Gln Ala Asp Lys Gly Lys Lys Gly Lys Asn Gly Lys Asn Gly  
 85 90 95  
 Gly Thr Asp Phe Thr Tyr Lys Thr Thr Tyr Thr Pro Lys Asn Asp Asp  
 100 105 110  
 Lys Asp Thr Lys Ala Gln Thr Gly Ala Ala Gly Ser Ser Gly Ala Gln  
 115 120 125  
 Thr Asp Leu Gly Lys Ala Asp Val Asn Gly Gly Lys Ala Glu Thr Lys  
 130 135 140  
 Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr Leu Lys Tyr  
 145 150 155 160  
 Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln Ala Gly Gly  
 165 170 175  
 Asn Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln Val Glu Gln Ser Met  
 180 185 190  
 Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro Asn Asp Gln  
 195 200 205  
 Asn Val Val  
 210

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: N. meningitidis
- (B) STRAIN: 1610

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Lys Arg Asp Lys Ala Glu Ser Gly Gly Gly Asn Gly Ala Ser Gly Gly  
 1 5 10 15  
 Thr Asp Ala Ala Ala Ser Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn  
 20 25 30



Ala Ala Ala Ser Asn Gly Ala Ala Gly Thr Ser Ser Glu Asn Gly Lys  
20 25 30

Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr Leu Asn Asp Lys Lys  
35 40 45

Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Ala  
50 55 60

Gly Ile Met Ile Pro Leu Met Pro Glu Thr Ser Glu Ser Gly Asn Asn  
65 70 75 80

Gln Ala Asp Leu Gly Leu Asn Gly Gly Thr Ala Phe Thr Arg Lys Phe  
85 90 95

Asp His Thr Pro Lys Ser Asp Glu Lys Asp Thr Gln Ala Gly Thr Pro  
100 105 110

Thr Asn Gly Ala Gln Thr Ala Ser Gly Thr Ala Gly Val Thr Gly Gly  
115 120 125

Gln Ala Gly Lys Thr Tyr Ala Val Glu Val Cys Cys Ser Asn Leu Asn  
130 135 140

Tyr Leu Lys Thr Gly Leu Leu Thr Arg Lys Thr Ala Asp Asn Thr Val  
145 150 155 160

Gly Ser Gly Asn Gly Ser Ser Thr Ala Ala Ala Gln Thr Ala Gln Gly  
165 170 175

Ala Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile  
180 185 190

Pro Lys Glu Gln Gln Asp Ile Val  
195 200

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: N. meningitidis
- (B) STRAIN: S3032

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Thr Lys Asp Lys Pro Ala Asn Gly Asn Thr Ala Glu Ala Ser Gly Gly  
 1 5 10 15  
 Thr Asp Ala Ala Ala Ser Gly Gly Ala Ala Gly Thr Ser Ser Glu Asn  
 20 25 30  
 Ser Lys Leu Thr Thr Val Leu Asp Ala Val Glu Leu Thr His Gly Gly  
 35 40 45  
 Thr Ala Ile Lys Asn Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val  
 50 55 60  
 Val Asp Gly Ile Met Ile Pro Leu Leu Pro Gln Asn Ser Thr Gly Lys  
 65 70 75 80  
 Asn Asn Gln Pro Asp Gln Gly Lys Asn Gly Gly Thr Ala Phe Ile Tyr  
 85 90 95  
 Leu Thr Thr Tyr Thr Pro Lys Asn Asp Asp Lys Asp Thr Lys Ala Gln  
 100 105 110  
 Thr Val Thr Gly Gly Thr Gln Thr Ala Ser Asn Thr Ala Gly Asp Ala  
 115 120 125  
 Asn Gly Lys Thr Lys Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu  
 130 135 140  
 Asn Tyr Leu Lys Thr Gly Leu Leu Thr Arg Lys Thr Ala Gly Asn Thr  
 145 150 155 160  
 Val Gly Ser Gly Asn Ser Ser Pro Thr Ala Ala Ala Gln Thr Asp Ala  
 165 170 175  
 Gln Ser Met Phe Leu Gln Gly Glu Arg Thr Asp Glu Asn Lys Ile Pro  
 180 185 190  
 Ser Glu Gln Asn Val Val  
 195

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: N. meningitidis
- (B) STRAIN: 891

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Thr Lys Asp Lys Pro Gly Asn Gly Ala Arg Leu Gln Ala Ala Arg Cys  
1 5 10 15  
Gly Thr Ser Asn Gly Ala Ala Gly Gln Ser Ser Glu Asn Ser Lys Leu  
20 25 30  
Thr Thr Val Leu Asp Ala Val Glu Leu Lys Leu Gly Asp Lys Glu Val  
35 40 45  
Gln Lys Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp Gly  
50 55 60  
Ile Met Ile Pro Leu Leu Pro Lys Asp Ser Glu Ser Gly Lys Asn Gln  
65 70 75 80  
Ala Asp Lys Gly Lys Asn Gly Glu Thr Glu Phe Thr Arg Lys Phe Glu  
85 90 95  
His Thr Pro Glu Ser Asp Glu Lys Asp Ala Gln Ala Gly Thr Pro Ser  
100 105 110  
Asn Gly Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly Lys  
115 120 125  
Thr Lys Thr Tyr Glu Val Asn Leu Cys Ser Asn Leu Asn Tyr Leu Lys  
130 135 140  
Tyr Gly Leu Leu Thr Arg Lys Thr Ala Gly Asn Thr Gly Glu Gly Gly  
145 150 155 160  
Asn Ser Ser Pro Thr Ala Ala Gln Thr Ala Gln Gly Ala Gln Ser Met  
165 170 175  
Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro Asn Asp Gln  
180 185 190  
Asn Val Val  
195

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

AAACCCGGAT CCGTTGCCAG CGCTGCCGT



(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TTTTTTCATG AGATATCTGG CAACATTGTT GTTATCTCTG GCGGTGTTAA TCACCGCCGG 60  
GTGCCTGGGT GGC GGCGGCA GTTTC 85

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GTGTTTTTGT TGAGTGCATG CCTGGGTGGC 30

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TGCGCAAGCT TACAGTTTGT CTTTGGTTTT CGCGCTGCCG 40

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

AAAAAGCATG CATAAAACT ACGCGTTACA CCATTCAAGC

40

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

*B'*  
*cat* (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TATATAAGCT TACGTTGCAG GCCCTGCCGC GTTTTCCCC

39

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CCCGAATTCT GCCGTCTGAA GCCTTATTC

29

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CCCGAATTCT GCTATGGTGC TGCCTGTG

28

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CGCATCCAAA ACCGTACCTG TGCTGCCTGA

30

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

TTTATCACTT TCCGGGGGCA GGAGCGGAAT

30

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GTTGGAACAG CAGACAGCGG TTTGCGCCCC

30

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GAACATACTT TGTTGTTTT TGC GCGTCAA

30

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

*b'*  
*cont.* (vi) ORIGINAL SOURCE:

- (A) ORGANISM: N. meningitidis
- (B) STRAIN: IM2394

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Tyr Lys Gly Thr Trp  
1 5

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: N. meningitidis
- (B) STRAIN: IM2394

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Glu Phe Glu Val Asp Phe Ser Asp Lys Thr Ile Lys Gly Thr Leu  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: N. meningitidis
- (B) STRAIN: IM2394

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Glu Gly Gly Phe Tyr Gly Pro Lys Gly Glu Glu Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- B' cont.
- (A) LENGTH: 6 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: N. meningitidis
- (B) STRAIN: IM2394

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Ala Val Phe Gly Ala Lys  
1 5

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2125 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..2067

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: 1..60

(ix) FEATURE:

(A) NAME/KEY: mat\_peptide

(B) LOCATION: 61..2067

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

ATG AAC AAT CCA TTG GTA AAT CAG GCT GCT ATG GTG CTG CCT GTG TTT	48
Met Asn Asn Pro Leu Val Asn Gln Ala Ala Met Val Leu Pro Val Phe	
-20 -15 -10 -5	
TTG TTG AGT GCT TGT CTG GGC GGA GGC GGC AGT TTC GAT CTT GAT TCT	96
Leu Leu Ser Ala Cys Leu Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser	
1 5 10	
GTC GAT ACC GAA GCC CCG CGT CCC GCG CCA AAG TAT CAA GAT GTT TCT	144
Val Asp Thr Glu Ala Pro Arg Pro Ala Pro Lys Tyr Gln Asp Val Ser	
15 20 25	
TCC GAA ACA CCG CAA GCC CAA AAA GAC CAA GGC GGA TAC GGT TTT GCA	192
Ser Glu Thr Pro Gln Ala Gln Lys Asp Gln Gly Gly Tyr Gly Phe Ala	
30 35 40	
ATG CGC TTC AAG CGG CGG AAT TGG TAC CCA AAA AAT GAA GAA GAT CAT	240
Met Arg Phe Lys Arg Arg Asn Trp Tyr Pro Lys Asn Glu Glu Asp His	
45 50 55 60	
AAG GCA TTA TCA GAA GCG GAT TGG GAG AAG TTA GGT GCG GGT AAG CCA	288
Lys Ala Leu Ser Glu Ala Asp Trp Glu Lys Leu Gly Ala Gly Lys Pro	
65 70 75	
GAT GAG TTT CCC CAA AGG AAT GAA ATA TTG AAT ATG ACT GAC GGA ATT	336
Asp Glu Phe Pro Gln Arg Asn Glu Ile Leu Asn Met Thr Asp Gly Ile	
80 85 90	
CTG AGT GAG TCT CTT CAG CTG GGT GAG GGC GGC AAA AGC CGC GTA GAA	384
Leu Ser Glu Ser Leu Gln Leu Gly Glu Gly Gly Lys Ser Arg Val Glu	
95 100 105	
GGA TAC ACG GAT TTC CAA TAT GTC CGC TCG GGC TAT ATC TAC CGC AAC	432
Gly Tyr Thr Asp Phe Gln Tyr Val Arg Ser Gly Tyr Ile Tyr Arg Asn	
110 115 120	

GGT Gly 125	GCC Ala	AAT Asn	AAA Lys	ATC Ile	GAT Asp 130	TTC Phe	CAA Gln	AAA Lys	AAA Lys	ATC Ile 135	GCC Ala	CTT Leu	TCC Ser	GGT Gly	CCG Pro 140	480
GAC Asp	GGC Gly	TAC Tyr	CTT Leu	TTC Phe 145	TAC Tyr	AAA Lys	GGC Gly	AGC Ser	AAT Asn 150	CCT Pro	TCC Ser	CAA Gln	GCT Ala	CTG Leu 155	CCG Pro	528
ATG Met	GGT Gly	AAG Lys	GTA Val 160	GGT Gly	TAT Tyr	AAA Lys	GGT Gly	ACT Thr 165	TGG Trp	GAT Asp	TAT Tyr	GTA Val	ACC Thr 170	GAT Asp	GCC Ala	576
AAG Lys	ATG Met	GGA Gly 175	CAA Gln	AAA Lys	TTT Phe	TCC Ser	CAG Gln 180	TTG Leu	GCT Ala	GGT Gly	TTT Phe	CCA Pro 185	GCG Ala	GGG Gly	GAT Asp	624
AGG Arg 190	TAT Tyr	GGG Gly	GCT Ala	TTG Leu	TCT Ser	GCC Ala 195	GAG Glu	GAA Glu	GCG Ala	GAT Asp	GTG Val 200	TTG Leu	CGC Arg	AAC Asn	AAA Lys	672
AGC Ser 205	GAG Glu	GCA Ala	CAG Gln	CAA Gln 210	GGT Gly	CAG Gln	ACC Thr	GAT Asp	TTC Phe	GGG Gly 215	CTG Leu	ACC Thr	AGC Ser	GAG Glu	TTT Phe 220	720
GAG Glu	GTG Val	GAT Asp	TTC Phe 225	GCC Ala	GCC Ala	AAG Lys	ACC Thr	ATG Met	ACC Thr 230	GGC Gly	GCG Ala	CTC Leu	TAC Tyr	CGC Arg 235	AAT Asn	768
AAC Asn	CGG Arg	ATT Ile	ACT Thr 240	AAT Asn	AAC Asn	GAA Glu	ACC Thr	GAA Glu 245	AAT Asn	AAA Lys	GCC Ala	AAA Lys	CAA Gln 250	ATT Ile	AAA Lys	816
CGT Arg	TAC Tyr	GAC Asp 255	ATT Ile	CAG Gln	GCT Ala	GAC Asp	CTG Leu 260	CAC His	GGT Gly	AAC Asn	CGC Arg	TTC Phe 265	AGC Ser	GGC Gly	AAG Lys	864
GCA Ala 270	ACG Thr	GCA Ala	ACC Thr	GAC Asp	AAA Lys	CCC Pro 275	AAA Lys	AAC Asn	GAC Asp	GAA Glu	ACC Thr 280	AAG Lys	GAA Glu	CAT His	CCC Pro	912
TTT Phe 285	GTT Val	TCC Ser	GAC Asp	TCG Ser 290	TCT Ser	TCT Ser	TTG Leu	AGC Ser	GGC Gly	GGC Gly 295	TTT Phe	TTC Phe	GGT Gly	CCG Pro 300	AAG Lys	960
GGT Gly	GAG Glu	GAA Glu	TTG Leu 305	GGT Gly	TTC Phe	CGC Arg	TTT Phe	TTG Leu 310	AGC Ser	GAC Asp	GAT Asp	CAA Gln	AAA Lys	GTT Val 315	GCC Ala	1008
GTT Val	GTC Val	GCC Gly 320	AGC Ser	GCG Ala	AAA Lys	ACC Thr	AAA Lys	GAC Asp 325	AAA Lys	CTG Leu	GAA Glu	AAT Asn	GGC Gly 330	GCG Ala	GCG Ala	1056

8' only.

GCT	TCA	GGC	AGC	ACA	GGT	GCG	GCA	GCA	TCG	GGC	GGT	GCG	GCA	GAT	ATG	1104
Ala	Ser	Gly	Ser	Thr	Gly	Ala	Ala	Ala	Ser	Gly	Gly	Ala	Ala	Asp	Met	
		335						340					345			
CCG	TCT	GAA	AAC	GGT	AAG	CTG	ACC	ACG	GTT	TTG	GAT	GCG	GTT	GAG	CTG	1152
Pro	Ser	Glu	Asn	Gly	Lys	Leu	Thr	Thr	Val	Leu	Asp	Ala	Val	Glu	Leu	
		350				355					360					
AAA	TCT	GGC	GGT	AAG	GAA	GTC	AAA	AAT	CTC	GAC	AAC	TTC	AGC	AAT	GCC	1200
Lys	Ser	Gly	Gly	Lys	Glu	Val	Lys	Asn	Leu	Asp	Asn	Phe	Ser	Asn	Ala	
		365			370					375					380	
GCC	CAA	CTG	GTT	GTC	GAC	GGC	ATT	ATG	ATT	CCG	CTC	CTG	CCC	AAG	AAT	1248
Ala	Gln	Leu	Val	Val	Asp	Gly	Ile	Met	Ile	Pro	Leu	Leu	Pro	Lys	Asn	
				385					390					395		
TCC	GAA	AGC	GAG	AGC	AAT	CAG	GCA	GAT	AAA	GGT	AAA	AAC	GGC	GGA	ACA	1296
Ser	Glu	Ser	Glu	Ser	Asn	Gln	Ala	Asp	Lys	Gly	Lys	Asn	Gly	Gly	Thr	
			400					405					410			
GCC	TTT	ACC	CGC	AAA	TTT	GAA	CAC	ACG	CCG	GAA	AGT	GAT	AAA	AAA	GAC	1344
Ala	Phe	Thr	Arg	Lys	Phe	Glu	His	Thr	Pro	Glu	Ser	Asp	Lys	Lys	Asp	
		415					420					425				
ACC	CAA	GCA	GGT	ACG	GCG	GAG	AAT	GGC	AAT	CCA	GCC	GCT	TCA	AAT	ACG	1392
Thr	Gln	Ala	Gly	Thr	Ala	Glu	Asn	Gly	Asn	Pro	Ala	Ala	Ser	Asn	Thr	
		430				435					440					
GCA	GGT	GAT	ACC	AAT	GGC	AAA	ACA	AAA	ACC	TAT	GAA	GTC	GAA	GTC	TGC	1440
Ala	Gly	Asp	Thr	Asn	Gly	Lys	Thr	Lys	Thr	Tyr	Glu	Val	Glu	Val	Cys	
		445			450					455					460	
TGT	TCC	AAC	CTC	AAT	TAT	CTG	AAA	TAC	GGA	ATG	TTG	ACG	CGT	AAA	AAC	1488
Cys	Ser	Asn	Leu	Asn	Tyr	Leu	Lys	Tyr	Gly	Met	Leu	Thr	Arg	Lys	Asn	
				465					470					475		
AGC	AAG	TCC	GCG	ATG	CAG	GCA	GGC	GAA	AAC	GGT	AGT	CTA	GCT	GAC	GCT	1536
Ser	Lys	Ser	Ala	Met	Gln	Ala	Gly	Glu	Asn	Gly	Ser	Leu	Ala	Asp	Ala	
			480					485					490			
AAA	ACG	GAA	CAA	GTT	GAA	CAA	AGT	ATG	TTC	CTC	CAA	GGC	GAG	CGC	ACC	1584
Lys	Thr	Glu	Gln	Val	Glu	Gln	Ser	Met	Phe	Leu	Gln	Gly	Glu	Arg	Thr	
		495					500					505				
GAT	GAA	AAA	GAG	ATT	CCA	AAA	GAG	CAA	CAA	GAC	ATC	GTT	TAT	CGG	GGG	1632
Asp	Glu	Lys	Glu	Ile	Pro	Lys	Glu	Gln	Gln	Asp	Ile	Val	Tyr	Arg	Gly	
		510				515					520					
TCT	TGG	TAC	GGG	CAT	ATT	GCC	AAC	GAC	ACA	AGC	TGG	AGC	GGC	AAT	GCT	1680
Ser	Trp	Tyr	Gly	His	Ile	Ala	Asn	Asp	Thr	Ser	Trp	Ser	Gly	Asn	Ala	
					530					535					540	

B  
cont.



TCA	GAT	AGA	GAG	GGC	GGC	AAC	AGG	GCG	GAC	TTT	ACC	GTG	AAT	TTT	GGT	1728
Ser	Asp	Arg	Glu	Gly	Gly	Asn	Arg	Ala	Asp	Phe	Thr	Val	Asn	Phe	Gly	
			545						550					555		
ACG	AAA	AAA	ATT	AAC	GGA	ACG	TTA	ACC	GCT	GAA	AAC	AGG	CAG	GAG	GCA	1776
Thr	Lys	Lys	Ile	Asn	Gly	Thr	Leu	Thr	Ala	Glu	Asn	Arg	Gln	Glu	Ala	
			560					565					570			
ACC	TTT	ACC	ATT	GTG	GGC	GAT	ATT	AAG	GAC	AAC	GGC	TTT	GAA	GGT	ACG	1824
Thr	Phe	Thr	Ile	Val	Gly	Asp	Ile	Lys	Asp	Asn	Gly	Phe	Glu	Gly	Thr	
		575					580					585				
GCG	AAA	ACT	GCT	GAC	TCA	GGT	TTT	GAT	CTC	GAT	CAA	AGC	AAT	ACC	ACC	1872
Ala	Lys	Thr	Ala	Asp	Ser	Gly	Phe	Asp	Leu	Asp	Gln	Ser	Asn	Thr	Thr	
	590					595					600					
CGC	ACG	CCT	AAG	GCA	TAT	ATC	ACA	GAT	GCC	AAG	GTG	AAG	GGC	GGT	TTT	1920
Arg	Thr	Pro	Lys	Ala	Tyr	Ile	Thr	Asp	Ala	Lys	Val	Lys	Gly	Gly	Phe	
605					610					615					620	
TAC	GGG	CCT	AAA	GCC	GAA	GAG	TTG	GGC	GGA	TGG	TTT	GCC	TAT	CCG	GGC	1968
Tyr	Gly	Pro	Lys	Ala	Glu	Glu	Leu	Gly	Gly	Trp	Phe	Ala	Tyr	Pro	Gly	
				625					630					635		
GAT	AAA	CAA	ACG	GAA	AAG	GCA	ACG	GTT	ACA	TCC	GGC	GAT	GGA	AAT	TCA	2016
Asp	Lys	Gln	Thr	Glu	Lys	Ala	Thr	Val	Thr	Ser	Gly	Asp	Gly	Asn	Ser	
			640					645					650			
GCA	AGC	AGT	GCA	ACT	GTC	GTA	TTC	GGT	GCG	AAA	CGC	CAA	AAG	CCT	GTG	2064
Ala	Ser	Ser	Ala	Thr	Val	Val	Phe	Gly	Ala	Lys	Arg	Gln	Lys	Pro	Val	
		655					660					665				
CAA	TAAAGTTTCG	ATCTTGATTC	TGTCGATACC	GAAGCCCCGC	GTCCCGCGCC	AAATAAAA	2125									
Gln																

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 689 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Met	Asn	Asn	Pro	Leu	Val	Asn	Gln	Ala	Ala	Met	Val	Leu	Pro	Val	Phe	
-20					-15					-10					-5	
Leu	Leu	Ser	Ala	Cys	Leu	Gly	Gly	Gly	Gly	Ser	Phe	Asp	Leu	Asp	Ser	
				1				5					10			

Val Asp Thr Glu Ala Pro Arg Pro Ala Pro Lys Tyr Gln Asp Val Ser  
 15 20 25  
 Ser Glu Thr Pro Gln Ala Gln Lys Asp Gln Gly Gly Tyr Gly Phe Ala  
 30 35 40  
 Met Arg Phe Lys Arg Arg Asn Trp Tyr Pro Lys Asn Glu Glu Asp His  
 45 50 55 60  
 Lys Ala Leu Ser Glu Ala Asp Trp Glu Lys Leu Gly Ala Gly Lys Pro  
 65 70 75  
 Asp Glu Phe Pro Gln Arg Asn Glu Ile Leu Asn Met Thr Asp Gly Ile  
 80 85 90  
 Leu Ser Glu Ser Leu Gln Leu Gly Glu Gly Gly Lys Ser Arg Val Glu  
 95 100 105  
 Gly Tyr Thr Asp Phe Gln Tyr Val Arg Ser Gly Tyr Ile Tyr Arg Asn  
 110 115 120  
 Gly Ala Asn Lys Ile Asp Phe Gln Lys Lys Ile Ala Leu Ser Gly Pro  
 125 130 135 140  
 Asp Gly Tyr Leu Phe Tyr Lys Gly Ser Asn Pro Ser Gln Ala Leu Pro  
 145 150 155  
 Met Gly Lys Val Gly Tyr Lys Gly Thr Trp Asp Tyr Val Thr Asp Ala  
 160 165 170  
 Lys Met Gly Gln Lys Phe Ser Gln Leu Ala Gly Phe Pro Ala Gly Asp  
 175 180 185  
 Arg Tyr Gly Ala Leu Ser Ala Glu Glu Ala Asp Val Leu Arg Asn Lys  
 190 195 200  
 Ser Glu Ala Gln Gln Gly Gln Thr Asp Phe Gly Leu Thr Ser Glu Phe  
 205 210 215 220  
 Glu Val Asp Phe Ala Ala Lys Thr Met Thr Gly Ala Leu Tyr Arg Asn  
 225 230 235  
 Asn Arg Ile Thr Asn Asn Glu Thr Glu Asn Lys Ala Lys Gln Ile Lys  
 240 245 250  
 Arg Tyr Asp Ile Gln Ala Asp Leu His Gly Asn Arg Phe Ser Gly Lys  
 255 260 265  
 Ala Thr Ala Thr Asp Lys Pro Lys Asn Asp Glu Thr Lys Glu His Pro  
 270 275 280  
 Phe Val Ser Asp Ser Ser Ser Leu Ser Gly Gly Phe Phe Gly Pro Lys  
 285 290 295 300

Gly Glu Glu Leu Gly Phe Arg Phe Leu Ser Asp Asp Gln Lys Val Ala  
 305 310 315  
 Val Val Gly Ser Ala Lys Thr Lys Asp Lys Leu Glu Asn Gly Ala Ala  
 320 325 330  
 Ala Ser Gly Ser Thr Gly Ala Ala Ala Ser Gly Gly Ala Ala Asp Met  
 335 340 345  
 Pro Ser Glu Asn Gly Lys Leu Thr Thr Val Leu Asp Ala Val Glu Leu  
 350 355 360  
 Lys Ser Gly Gly Lys Glu Val Lys Asn Leu Asp Asn Phe Ser Asn Ala  
 365 370 375 380  
 Ala Gln Leu Val Val Asp Gly Ile Met Ile Pro Leu Leu Pro Lys Asn  
 385 390 395  
 Ser Glu Ser Glu Ser Asn Gln Ala Asp Lys Gly Lys Asn Gly Gly Thr  
 400 405 410  
 Ala Phe Thr Arg Lys Phe Glu His Thr Pro Glu Ser Asp Lys Lys Asp  
 415 420 425  
 Thr Gln Ala Gly Thr Ala Glu Asn Gly Asn Pro Ala Ala Ser Asn Thr  
 430 435 440  
 Ala Gly Asp Thr Asn Gly Lys Thr Lys Thr Tyr Glu Val Glu Val Cys  
 445 450 455 460  
 Cys Ser Asn Leu Asn Tyr Leu Lys Tyr Gly Met Leu Thr Arg Lys Asn  
 465 470 475  
 Ser Lys Ser Ala Met Gln Ala Gly Glu Asn Gly Ser Leu Ala Asp Ala  
 480 485 490  
 Lys Thr Glu Gln Val Glu Gln Ser Met Phe Leu Gln Gly Glu Arg Thr  
 495 500 505  
 Asp Glu Lys Glu Ile Pro Lys Glu Gln Gln Asp Ile Val Tyr Arg Gly  
 510 515 520  
 Ser Trp Tyr Gly His Ile Ala Asn Asp Thr Ser Trp Ser Gly Asn Ala  
 525 530 535 540  
 Ser Asp Arg Glu Gly Gly Asn Arg Ala Asp Phe Thr Val Asn Phe Gly  
 545 550 555  
 Thr Lys Lys Ile Asn Gly Thr Leu Thr Ala Glu Asn Arg Gln Glu Ala  
 560 565 570  
 Thr Phe Thr Ile Val Gly Asp Ile Lys Asp Asn Gly Phe Glu Gly Thr  
 575 580 585

Ala Lys Thr Ala Asp Ser Gly Phe Asp Leu Asp Gln Ser Asn Thr Thr  
590 595 600

Arg Thr Pro Lys Ala Tyr Ile Thr Asp Ala Lys Val Lys Gly Gly Phe  
605 610 615 620

Tyr Gly Pro Lys Ala Glu Glu Leu Gly Gly Trp Phe Ala Tyr Pro Gly  
625 630 635

Asp Lys Gln Thr Glu Lys Ala Thr Val Thr Ser Gly Asp Gly Asn Ser  
640 645 650

Ala Ser Ser Ala Thr Val Val Phe Gly Ala Lys Arg Gln Lys Pro Val  
655 660 665

Gln

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2143 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..2133

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 1..60

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 61..2133

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

ATG AAC AAT CCA TTG GTA AAT CAG GCT GCT ATG GTG CTG CCT GTG TTT	48
Met Asn Asn Pro Leu Val Asn Gln Ala Ala Met Val Leu Pro Val Phe	
-20 -15 -10 -5	
TTG TTG AGT GCT TGT TTG GGC GGA GGC GGC AGT TTC GAT CTT GAT TCT	96
Leu Leu Ser Ala Cys Leu Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser	
1 5 10	

GTC	GAT	ACC	GAA	GCC	CCG	CGT	CCC	GCG	CCA	AAA	TAT	CAA	GAT	GTT	TCT	144
Val	Asp	Thr	Glu	Ala	Pro	Arg	Pro	Ala	Pro	Lys	Tyr	Gln	Asp	Val	Ser	
	15						20					25				
TCC	GAA	AAA	CCG	CAA	GCC	CAA	AAA	GAC	CAA	GGC	GGA	TAC	GGT	TTT	GCG	192
Ser	Glu	Lys	Pro	Gln	Ala	Gln	Lys	Asp	Gln	Gly	Gly	Tyr	Gly	Phe	Ala	
	30					35					40					
ATG	AGG	TTG	AAA	CGG	AGG	AAT	CGG	CAT	CCG	CAG	GCA	AAA	GAA	GAC	AAA	240
Met	Arg	Leu	Lys	Arg	Arg	Asn	Arg	His	Pro	Gln	Ala	Lys	Glu	Asp	Lys	
	45				50					55					60	
GTT	GAA	CTA	AAC	CCA	AAT	GAT	TGG	GAG	GAG	ACA	GGA	TTG	CCG	AGC	AAG	288
Val	Glu	Leu	Asn	Pro	Asn	Asp	Trp	Glu	Glu	Thr	Gly	Leu	Pro	Ser	Lys	
				65				70						75		
CCC	CAA	AAC	TTA	CCC	GAG	CGA	CAG	CAA	TCG	GTT	ATT	GAT	AAA	GTA	AAA	336
Pro	Gln	Asn	Leu	Pro	Glu	Arg	Gln	Gln	Ser	Val	Ile	Asp	Lys	Val	Lys	
			80					85					90			
ACA	GAC	GAT	GGC	AGC	AAT	ATT	TAC	ACT	TCC	CCT	TAT	CTC	ACG	CAA	TCA	384
Thr	Asp	Asp	Gly	Ser	Asn	Ile	Tyr	Thr	Ser	Pro	Tyr	Leu	Thr	Gln	Ser	
	95						100					105				
AAC	CAT	CAA	AAC	GGC	AGC	ACT	AAT	AGC	GGT	GCA	AAC	CAA	CCA	AAA	AAC	432
Asn	His	Gln	Asn	Gly	Ser	Thr	Asn	Ser	Gly	Ala	Asn	Gln	Pro	Lys	Asn	
	110					115					120					
GAA	GTA	AAA	GAT	TAC	AAA	AAT	TTC	AAA	TAT	GTT	TAT	TCC	GGC	TGG	TTT	480
Glu	Val	Lys	Asp	Tyr	Lys	Asn	Phe	Lys	Tyr	Val	Tyr	Ser	Gly	Trp	Phe	
	125				130					135					140	
TAT	AAA	CAT	GCA	GAG	AGT	GAA	AGA	GAA	TTC	AGT	AAA	ATC	AAA	TTT	AAG	528
Tyr	Lys	His	Ala	Glu	Ser	Glu	Arg	Glu	Phe	Ser	Lys	Ile	Lys	Phe	Lys	
				145					150					155		
TCA	GGC	GAC	GAC	GGC	TAT	ATT	TTT	TAT	CAC	GGT	AAA	GAC	CCT	TCC	CGA	576
Ser	Gly	Asp	Asp	Gly	Tyr	Ile	Phe	Tyr	His	Gly	Lys	Asp	Pro	Ser	Arg	
				160				165					170			
CAA	CTT	CCC	ACT	TCT	GAA	AAA	GTT	ATC	TAC	AAA	GGC	GTA	TGG	CAT	TTT	624
Gln	Leu	Pro	Thr	Ser	Glu	Lys	Val	Ile	Tyr	Lys	Gly	Val	Trp	His	Phe	
		175					180					185				
GTA	ACC	GAT	ACT	GAA	AAG	GGA	CAA	AAA	TTT	AAC	GAT	ATT	CTT	GAA	ACC	672
Val	Thr	Asp	Thr	Glu	Lys	Gly	Gln	Lys	Phe	Asn	Asp	Ile	Leu	Glu	Thr	
	190					195					200					
TCA	AAA	GGG	CAA	GGC	GAC	AGA	TAC	AGC	GGA	TTT	TCG	GGC	GAT	GAC	GGC	720
Ser	Lys	Gly	Gln	Gly	Asp	Arg	Tyr	Ser	Gly	Phe	Ser	Gly	Asp	Asp	Gly	
	205				210					215					220	

GAA	ACA	ACT	TCC	AAT	AGA	ACT	GAT	TCC	AAC	CTT	AAT	GAT	AAG	CAC	GAG	768
Glu	Thr	Thr	Ser	Asn	Arg	Thr	Asp	Ser	Asn	Leu	Asn	Asp	Lys	His	Glu	
				225					230					235		
GGT	TAT	GGT	TTT	ACC	TCG	AAT	TTA	GAA	GTG	GAT	TTC	GGC	AGT	AAA	AAA	816
Gly	Tyr	Gly	Phe	Thr	Ser	Asn	Leu	Glu	Val	Asp	Phe	Gly	Ser	Lys	Lys	
			240					245					250			
TTG	ACG	GGT	AAA	TTA	ATA	CGC	AAT	AAT	AGA	GTT	ACA	AAC	GCT	ACT	ACT	864
Leu	Thr	Gly	Lys	Leu	Ile	Arg	Asn	Asn	Arg	Val	Thr	Asn	Ala	Thr	Thr	
		255					260					265				
AAC	GAT	AAA	TAC	ACC	ACC	CAA	TAC	TAC	AGC	CTT	GAT	GCC	CAA	ATA	ACA	912
Asn	Asp	Lys	Tyr	Thr	Thr	Gln	Tyr	Tyr	Ser	Leu	Asp	Ala	Gln	Ile	Thr	
	270					275					280					
GGC	AAC	CGC	TTC	AAC	GGT	AAG	GCG	ATA	GCG	ACC	GAC	AAA	CCC	GAC	ACT	960
Gly	Asn	Arg	Phe	Asn	Gly	Lys	Ala	Ile	Ala	Thr	Asp	Lys	Pro	Asp	Thr	
285				290					295						300	
GGA	GGA	ACC	AAA	CTA	CAT	CCC	TTT	GTT	TCC	GAC	TCG	TCT	TCT	TTG	AGC	1008
Gly	Gly	Thr	Lys	Leu	His	Pro	Phe	Val	Ser	Asp	Ser	Ser	Ser	Leu	Ser	
			305					310						315		
GGC	GGC	TTT	TTC	GGT	CCG	AAG	GGT	GAG	GAA	TTG	GGT	TTC	CGC	TTT	TTG	1056
Gly	Gly	Phe	Phe	Gly	Pro	Lys	Gly	Glu	Glu	Leu	Gly	Phe	Arg	Phe	Leu	
		320					325						330			
AGC	GAC	GAT	AAA	AAA	GTT	GCG	GTT	GTC	GGC	AGC	GCG	AAA	ACC	AAA	GAC	1104
Ser	Asp	Asp	Lys	Lys	Val	Ala	Val	Val	Gly	Ser	Ala	Lys	Thr	Lys	Asp	
		335				340					345					
AAA	ACG	GAA	AAT	GGC	GCG	GTG	GCT	TCA	GGC	GGC	ACA	GAT	GCG	GCA	GCA	1152
Lys	Thr	Glu	Asn	Gly	Ala	Val	Ala	Ser	Gly	Gly	Thr	Asp	Ala	Ala	Ala	
	350			355					360							
TCA	AAC	GGT	GCG	GCA	GGC	ACG	TCG	TCT	GAA	AAC	AGT	AAG	CTG	ACC	ACG	1200
Ser	Asn	Gly	Ala	Ala	Gly	Thr	Ser	Ser	Glu	Asn	Ser	Lys	Leu	Thr	Thr	
365				370					375						380	
GTT	TTG	GAT	GCG	GTC	GAG	CTG	AAA	TTG	GGC	GAT	AAG	GAA	GTC	CAA	AAG	1248
Val	Leu	Asp	Ala	Val	Glu	Leu	Lys	Leu	Gly	Asp	Lys	Glu	Val	Gln	Lys	
			385					390						395		
CTC	GAC	AAC	TTC	AGC	AAC	GCC	GCC	CAA	CTG	GTT	GTC	GAC	GGC	ATT	ATG	1296
Leu	Asp	Asn	Phe	Ser	Asn	Ala	Ala	Gln	Leu	Val	Val	Asp	Gly	Ile	Met	
			400				405						410			
ATT	CCG	CTC	TTG	CCC	GAG	ACT	TCC	GAA	AGT	GGG	AAC	AAT	CAA	GCC	AAT	1344
Ile	Pro	Leu	Leu	Pro	Glu	Thr	Ser	Glu	Ser	Gly	Asn	Asn	Gln	Ala	Asn	
		415					420					425				

CAA Gln 430	GGT Gly 430	ACA Thr 430	AAT Asn 430	GGC Gly 430	GGA Gly 435	ACA Thr 435	GCC Ala 435	TTT Phe 435	ACC Thr 435	CGC Arg 440	AAA Lys 440	TTT Phe 440	GAC Asp 440	CAC His 440	ACG Thr 440	1392
CCG Pro 445	GAA Glu 445	AGT Ser 445	GAT Asp 445	AAA Lys 450	AAA Lys 450	GAC Asp 450	GCC Ala 450	CAA Gln 450	GCA Ala 455	GGT Gly 455	ACG Thr 455	CAG Gln 455	ACG Thr 455	AAT Asn 460	GGG Gly 460	1440
GCG Ala 465	CAA Gln 465	ACC Thr 465	GCT Ala 465	TCA Ser 465	AAT Asn 465	ACG Thr 465	GCA Ala 470	GGT Gly 470	GAT Asp 470	ACC Thr 470	AAT Asn 475	GGC Gly 475	AAA Lys 475	ACA Thr 475	AAA Lys 475	1488
ACC Thr 480	TAT Tyr 480	GAA Glu 480	GTC Val 480	GAA Glu 480	GTC Val 480	TGC Cys 485	TGT Cys 485	TCC Ser 485	AAC Asn 485	CTC Leu 485	AAT Asn 490	TAT Tyr 490	CTG Leu 490	AAA Lys 490	TAC Tyr 490	1536
GGA Gly 495	ATG Met 495	TTG Leu 495	ACG Thr 495	CGC Arg 495	AAA Lys 495	AAC Asn 500	AGC Ser 500	AAG Lys 500	TCC Ser 500	GCG Ala 505	ATG Met 505	CAG Gln 505	GCA Ala 505	GGA Gly 505	GAA Glu 505	1584
AGC Ser 510	AGT Ser 510	AGT Ser 510	CAA Gln 510	GCT Ala 515	GAT Asp 515	GCT Ala 515	AAA Lys 515	ACG Thr 515	GAA Glu 520	CAA Gln 520	GTT Val 520	GGA Gly 520	CAA Gln 520	AGT Ser 520	ATG Met 520	1632
TTC Phe 525	CTC Leu 525	CAA Gln 525	GGC Gly 525	GAG Glu 530	CGC Arg 530	ACC Thr 530	GAT Asp 530	GAA Glu 535	AAA Lys 535	GAG Glu 535	ATT Ile 535	CCA Pro 535	AGC Ser 535	GAG Glu 540	CAA Gln 540	1680
AAC Asn 545	ATC Ile 545	GTT Val 545	TAT Tyr 545	CGG Arg 545	GGG Gly 545	TCT Ser 550	TGG Trp 550	TAC Tyr 550	GGG Gly 550	CAT His 550	ATT Ile 555	GCC Ala 555	AGC Ser 555	AGC Ser 555	ACA Thr 555	1728
AGC Ser 560	TGG Trp 560	AGC Ser 560	GGC Gly 560	AAT Asn 560	GCT Ala 565	TCT Ser 565	GAT Asp 565	AAA Lys 565	GAG Glu 570	GGC Gly 570	GGC Gly 570	AAC Asn 570	AGG Arg 570	GCG Ala 570	GAA Glu 570	1776
TTT Phe 575	ACT Thr 575	GTG Val 575	AAT Asn 575	TTT Phe 575	GGC Gly 580	GAG Glu 580	AAA Lys 580	AAA Lys 580	ATT Ile 585	ACC Thr 585	GGC Gly 585	ACG Thr 585	TTA Leu 585	ACC Thr 585	GCT Ala 585	1824
GAA Glu 590	AAC Asn 590	AGG Arg 590	CAG Gln 590	GAG Glu 595	GCA Ala 595	ACC Thr 595	TTT Phe 595	ACC Thr 595	ATT Ile 600	GAT Asp 600	GGT Gly 600	AAG Lys 600	ATT Ile 600	GAG Glu 600	GGC Gly 600	1872
AAC Asn 605	GGT Gly 605	TTT Phe 605	TCC Ser 610	GGT Gly 610	ACG Thr 610	GCA Ala 610	AAA Lys 615	ACT Thr 615	GCT Ala 615	GAA Glu 615	TTA Leu 615	GGT Gly 615	TTT Phe 615	GAT Asp 620	CTC Leu 620	1920
GAT Asp 625	CAA Gln 625	AAA Lys 625	AAT Asn 625	ACC Thr 625	ACC Thr 625	CGC Arg 630	ACG Thr 630	CCT Pro 630	AAG Lys 630	GCA Ala 635	TAT Tyr 635	ATC Ile 635	ACA Thr 635	GAT Asp 635	GCC Ala 635	1968

AAG GTG CAG GGC GGT TTT TAC GGG CCC AAA GCC GAA GAG TTG GGC GGA	2016
Lys Val Gln Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Leu Gly Gly	
640 645 650	
TGG TTT GCC TAT CAG GGC GAT AAA CAA ACG GAA AAT ACA ACA GTT GCA	2064
Trp Phe Ala Tyr Gln Gly Asp Lys Gln Thr Glu Asn Thr Thr Val Ala	
655 660 665	
TCC GGC AAT GGA AAT TCA GCA AGC AGT GCA ACT GTC GTA TTC GGT GCG	2112
Ser Gly Asn Gly Asn Ser Ala Ser Ser Ala Thr Val Val Phe Gly Ala	
670 675 680	
AAA CGC CAA AAG CCT GTG CAA TAAAGTAAAA	2143
Lys Arg Gln Lys Pro Val Gln	
685 690	

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 711 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Met Asn Asn Pro Leu Val Asn Gln Ala Ala Met Val Leu Pro Val Phe  
-20 -15 -10 -5

Leu Leu Ser Ala Cys Leu Gly Gly Gly Gly Ser Phe Asp Leu Asp Ser  
1 5 10

Val Asp Thr Glu Ala Pro Arg Pro Ala Pro Lys Tyr Gln Asp Val Ser  
15 20 25

Ser Glu Lys Pro Gln Ala Gln Lys Asp Gln Gly Gly Tyr Gly Phe Ala  
30 35 40

Met Arg Leu Lys Arg Arg Asn Arg His Pro Gln Ala Lys Glu Asp Lys  
45 50 55 60

Val Glu Leu Asn Pro Asn Asp Trp Glu Glu Thr Gly Leu Pro Ser Lys  
65 70 75

Pro Gln Asn Leu Pro Glu Arg Gln Gln Ser Val Ile Asp Lys Val Lys  
80 85 90

Thr Asp Asp Gly Ser Asn Ile Tyr Thr Ser Pro Tyr Leu Thr Gln Ser  
95 100 105

Asn His Gln Asn Gly Ser Thr Asn Ser Gly Ala Asn Gln Pro Lys Asn  
110 115 120